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(54) New embodiments of the HIV principal neutralizing determinant.

(57) New amino acid sequences of an envelope fragment of HIV are disclosed, as well as immunological conjugates for immunological purposes, including vaccination against AIDS.

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Acquired Immune Deficiency Syndrome (AIDS) is the clinical manifestation of the apparent infection of CD4 helper T-cells and other cell targets by human immunodeficiency virus (HIV), also previously referred to as human T-lymphotropic virus type III (HTLV-III), Lymphadenopathy-associated virus (LAV), or AIDS-related virus (ARV) (hereinafter collectively "HIV"). AIDS is a transmissible deficiency of cellular immunity characterized by opportunistic infections and certain malignancies. A similar disease, AIDS-related complex (ARC), shares many of the epidemiological features and immune abnormalities with AIDS, and often precedes the clinical manifestations of AIDS.

A vaccine against AIDS and/or ARC is an ideal prophylactic treatment for preventing the debilitating effects of infection by HIV. Applicants have discovered new immunogens useful for such a vaccine. The immunogens are new principal neutralizing determinants (PNDs) of HIV.

Many of the details of the genetic function and virion structure of HIV have not yet been elucidated. However, certain general features have emerged. An RNA virus with a genome totaling about 9 kilobases (kb), its nucleotide sequence contains seven major open reading frames (ORFs) corresponding to the gag, pol and env, vif, tat, rev, and nef genes. The genes gag, pol and env code respectively for core subunits, viral enzymes such as reverse transcriptase or protease, and outer surface subunits. The gene vif codes for a viral infectivity factor, which is a protein involved with enhancement of cell-to-cell transmission of virions without affecting the budding process. The gene tat codes for a small protein that transactivates the expression of all viral proteins. The gene rev regulates expression of the viral proteins of gag, pol and env genes, possibly by facilitating transport of incompletely spliced RNA. The nef gene codes for a viral protein found in the cell cytoplasm, and it may modulate the host cellular signaling system and serve as a transcriptional silencer. Terminal repeats in the nucleotide sequence are common to many retroviruses such as HIV and are required for viral replication and integration into the host chromosome. More recent discussions on the general nature of HIV genomic structure, replication and regulation are found in Ratner, L. et al. "Human T-Lymphotropic Retroviruses," in O'Brien, S.J. (ed.) *Genetic Maps 1987* Cold Spring Harbor 1987 pp. 124-129; Franchini, G. et al., *Nature* 328, 539 (1987); Varmus, H. *Genes & Dev* 2, 1055 (1988).

Principal neutralizing determinants (PNDs) have been located within a selected, conserved region of the env gene. These PNDs are still undefined. Applicants have discovered and defined new embodiments of PND.

AIDS is a disease of a virus with a unique collection of attributes. HIV itself targets the immune system; it possesses a reverse transcriptase capable of turning out highly mutated progeny; it is sequestered from the immune system and it has a hypervariable surface in the (env) region. See, e.g. Hilleman, M.R., *Vaccine* 6, 175 (1988); Barnes, D.M., *Science* 240, 719 (1988). In view of these attributes, it was neither anticipated nor expected that the principal neutralizing determinants of this invention would serve as effective AIDS immunogens.

BRIEF DESCRIPTION OF THE INVENTION

New principal neutralizing determinants of HIV are disclosed, and are useful as immunogens for AIDS vaccines, particularly in the form of conjugates

ABBREVIATIONS AND DEFINITIONS

AIDS	Acquired immune deficiency syndrome
ARC	AIDS-related complex
conjugation	The process of covalently attaching 2 molecules each containing one or more immunological determinants, e.g., HIV envelope fragments and Omp
conjugate,	Result of conjugation, also known as an antigenic conjugate or immunological conjugate
HIV	Generic term for the presumed etiological agent of AIDS and/or ARC, also referred to as strains HTLV-III, LAV, and ARV.
PND	Principal neutralization determinant of HIV
Omp	Outer membrane proteosome
Recombinant protein	A polypeptide or oligopeptide expressed by foreign DNA in a recombinant eukaryotic or prokaryotic expression system.
Recombinant expression system	A cell containing a foreign DNA expressing a foreign protein or a foreign oligopeptide.

Amino Acids			
	Full Name	Three-letter symbol	One-letter symbol
5	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
10	Asn and/or Asp	Asx	B
	Cysteine	Cys	C
	Glutamine	Gln	Q
	Glutamic acid	Glu	E
	Gln and/or Glu	Glx	Z
15	Glycine	Gly	G
	Histidine	His	H
	Isoleucine	Ile	I
	Leucine	Leu	L
	Lysine	Lys	K
20	Methionine	Met	M
	Phenylalanine	Phe	F
	Proline	Pro	P
	Serine	Ser	S
	Threonine	Thr	T
25	Tryptophan	Trp	W
	Tyrosine	Tyr	Y
	Valine	Val	V

Nucleotides Bases in DNA or RNA		
	Name	One-letter symbol
30	Adenine	A
	Cytosine	C
35	guanine	G
	thymine	T
	uracil	U

40 The terms "protein," "peptide," "oligopeptide," and "polypeptide" and their plurals have been used interchangeably to refer to chemical compounds having amino acid sequences of five or more amino acids. "Amino acid" refers to any of the 20 common amino acids for which codons are naturally available, and are listed in the table of amino acids given above.

45 When any variable (e.g. PND) occurs more than one time in any constituent or in Formula I, its definition on each occurrence is independent of its definition at every other occurrence. Also, combinations of substituents and/or variables are permissible only if such combinations result in stable compounds.

DETAILED DESCRIPTION OF THE INVENTION

50 The present invention provides an effective immunogen against AIDS or ARC, and comprises an antigenic conjugate of the formula



55 wherein:

PND is the principal neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n = 1-50, wherein n is the number of polypeptides of PND covalently linked to Omp;

~ indicates covalent linkage;

Omp is outer membrane proteosome of the microorganism Neisseria; said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine.

5 The antigenic conjugates of this invention are prepared by isolating and purifying their component parts PND and Omp, then conjugating PND and Omp together. Subsequent purification of conjugate mixtures may be performed as desired.

The new PND amino acid sequences of this invention include any fragment thereof, provided said fragment is at least five amino acids in length.

10 Each PND amino acid sequence is determined by DNA sequencing of HIV clones amplified by the polymerase chain reaction.

Polymerase Chain Reaction Amplification

15 Large amounts of DNA coding for PND protein may be obtained using polymerase chain reaction (PCR) amplification techniques as described in Mullis et al., U.S. Patent No. 4,800,159 and other published sources. See also, for example, Innis, M.A. et al. PCR Protocols Academic Press 1990. The extension product of one primer, when hybridized to another primer, becomes a template for the synthesis of another nucleic acid molecule.

20 The primer template complexes act as substrate for DNA polymerase which, in performing its replication function, extends the primers. The region in common with both primer extensions, upon denaturation, serves as template for a repeated primer extension.

25 Taq DNA Polymerase catalyzes primer extension in the amplification process. The enzyme is a thermostable DNA polymerase isolated from Thermus aquaticus. Because it stays active through repeated elevations to high denaturation temperatures, it needs to be added only once. Deoxynucleotide triphosphates provide the building blocks for primer extension.

30 The nucleic acid sequence strands are heated until they separate, in the presence of oligonucleotide primers that bind to their complementary strand at a particular site of the template. This process is continued with a series of heating and cooling cycles, heating to separate strands, and cooling to reanneal and extend the sequences. More and more copies of the strands are generated as the cycle is repeated. Through amplification, the coding domain and any additional primer-encoded information such as restriction sites or translation signals (signal sequences, start codons and/or stop codons) is obtained. PCR protocols are often performed at the 100 μ L scale in 0.5 ml microcentrifuge tubes. The PCR sample may be single- or double-stranded DNA or RNA. If the starting material is RNA, reverse transcriptase is used to prepare first 35 strand cDNA prior to PCR. Typically, nanogram amounts of cloned template, up to microgram amounts of genomic DNA, or 20,000 target copies are chosen to start optimization trials.

40 PCR primers are oligonucleotides, typically 15 to 50 bases long, and are complementary to sequences defining the 5' ends of the complementary template strands. Non-template complementary 5' extensions may be added to primers to allow a variety of useful post amplification operations on the PCR product without significant perturbation of the amplification itself. It is important that the two PCR primers not contain 45 more than two bases complementary with each other, especially at their 3' ends. Internal secondary structure should be avoided in primers.

Because Taq DNA Polymerase has activity in the 37-55°C range, primer extension will occur during the annealing step and the hybrid will be stabilized. The concentrations of the primers are preferably equal in conventional PCR and, typically, are in vast excess of the template to be reproduced.

In one typical PCR protocol, each deoxynucleotide triphosphate concentration is preferably about 200 μ M. The four dNTP concentrations are preferably above the estimated Km of each dNTP (10-15 μ M).

Preferably PCR buffer is composed of about 500 mM potassium chloride, 10.0 mM Tris-HCl (pH 8.3 at room temperature), 1.5 mM magnesium chloride, and 0.01% w/v gelatin. In the presence of 0.8 mM total 50 dNTP concentration, a titration series in small increments over the 1.5-to 4-mM range will locate the magnesium concentration producing the highest yield of a specific product. Too little free magnesium will result in no PCR product and too much free magnesium may produce a variety of unwanted products.

55 Preferably, in a 100- μ L reaction volume, 2.0 to 2.5 units of Taq DNA Polymerase are recommended. The enzyme can be added conveniently to a fresh master mix prepared for a number of reactions, thereby avoiding accuracy problems associated with adding individual 0.5- μ L enzyme aliquots to each tube. A typical PCR protocol for amplification of the DNA template includes a 1 minute 94°C denaturation step, a 1 minute 37°C primer annealing step, and a 2 minute 72°C primer extension step. This will amplify a 500 base-pair product at least 100,000-fold in 25 cycles.

During DNA denaturation, sufficient time must be allowed for thermal equilibration of the sample. The practical range of effective denaturation temperatures for most samples is 92-95°C, with 94°C being the standard choice.

Primer annealing is usually performed first at 37°C, and the specificity of the product is evaluated. If

- 5 unwanted bands are observed, the annealing temperature should be raised in subsequent optimization runs. While the primer annealing temperature range is often 37-55°C, it may be raised as high as the extension temperature in some cases. Merging of the primer annealing and primer extension steps results in a two-step PCR process.

- 10 Primer extension, in most applications, occurs effectively at a temperature of 72°C and seldom needs optimization. In the two-temperature PCR process the temperature range may be 65-70°C. In situations where enzyme concentration limits amplification in late cycles, the extension is preferably increased linearly with cyclic number. Usually, 25 to 45 cycles are required for extensive amplification (i.e., 1,000,000 fold) of a specific target.

- 15 Once the DNA sequence is determined, through conventional and well-known techniques, its amino acid sequence can be deduced by "translating" the DNA sequence. The resulting amino acid sequence having the principal neutralizing determinant of the envelope gene is then employed to synthesize large quantities of PND protein or fragment thereof. Synthesis is performed by organic synthesis or by recombinant expression systems, or both.

20 Preparation of Principal Neutralization Determinant

A. Organic Synthesis of PND:

- Standard and conventional methods exist for rapid and accurate synthesis of long peptides on solid-phase supports. Solution-phase synthesis is usually feasible only for selected smaller peptides.

- 25 Synthesis on solid-phase supports, or solid-phase synthesis, is most conveniently performed on an automated peptide synthesizer according to e.g., Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al., (eds.), Synthetic Peptides in Biology and Medicine, Elsevier 1985, pp. 29-57. Manual solid-phase synthesis may be employed instead, by following 30 the classical Merrifield techniques, as described, for example, in Merrifield, R.B. J. Am. Chem. Soc. 85, 2149 (1963), or known improvements thereof. Solid-phase peptide synthesis may also be performed by the Fmoc method, which employs very dilute base to remove the Fmoc protecting group. Segment synthesis-condensation is a further variant of organic synthesis of peptides as within the scope of the techniques of the present invention.

- 35 In organic synthesis of peptides, protected amino acids are condensed to form amide or peptide bonds with the N-terminus of a growing peptide. Condensation is usually performed with the carbodiimide method by reagents such as dicyclohexylcarbodiimide, or N-ethyl, N₁-(γ -dimethylaminopropyl) carbodiimide. Other methods of forming the amide or peptide bond include, but are not limited to, synthetic routes via an acid chloride, azide, mixed anhydride or activated ester. Common solid-phase supports include polystyrene or 40 polyamide resins.

- The selection of protecting groups of amino acid side chains is, in part, dictated by particular coupling conditions, in part by the amino acid and peptide components involved in the reaction. Such amino-protecting groups ordinarily employed include those which are well known in the art, for example, urethane-protecting substituents such as benzyloxycarbonyl (carbobenzoxy), p-methoxycarbobenzoxy, p-nitrocarbobenzoxy, t-butyloxycarbonyl, and the like. It is preferred to utilize t-butoxycarbonyl (BOC) for protecting the ϵ -amino group, in part because the BOC protecting group is readily removed by relatively mild acids such as trifluoroacetic acid (TFA), or hydrogen chloride in ethyl acetate.

- 45 The OH group of Thr and Ser may be protected by the Bzl (benzyl) group and the ϵ -amino group of Lys may be protected by the isopropoxycarbonyl (IPOC) group or the 2-chlorobenzylloxycarbonyl (2-Cl-CBZ) group. Treatment with HF or catalytic hydrogenation are typically employed for removal of IPOC or 2-Cl-CBZ.

- 50 For preparing cocktails of closely related peptides, see, e.g., Houghton, R.A., Proc. Natl. Acad. Sci. USA 82, 5131 (1985).

55 B. Expression of PND in a Recombinant Expression System

- It is now a relatively straightforward technology to prepare cells expressing a foreign gene. Such cells act as hosts and include E. coli, B. subtilis, yeasts, fungi, plant cells or animal cells. Expression vectors for

many of these host cells have been isolated and characterized, and are used as starting materials in the construction, through conventional recombinant DNA techniques, of vectors having a foreign DNA insert of interest. Any DNA is foreign if it does not naturally derive from the host cells used to express the DNA insert. The foreign DNA insert may be expressed on extrachromosomal plasmids or after integration in whole or in part in the host cell chromosome(s), or may actually exist in the host cell as a combination of more than one molecular form. The choice of host cell and expression vector for the expression of a desired foreign DNA largely depends on availability of the host cell and how fastidious it is, whether the host cell will support the replication of the expression vector, and other factors readily appreciated by those of ordinary skill in the art.

10 The technology for recombinant prokaryotic expression systems is now old and conventional. The typical host cell is *E. coli*. The technology is illustrated by treatises such as Wu, R (ed) *Meth. Enzymol.* 68 - (1979) and Maniatis, T. et. al., *Molecular Cloning: A Laboratory Manual* Cold Spring Harbor 1982.

The foreign DNA insert of interest comprises any DNA sequence coding for a PND (or fragment thereof of at least 5 amino acids in length) of the present invention, including any synthetic sequence with this coding capacity or any such cloned sequence or combination thereof. For example, PND peptide coded and expressed by an entirely recombinant DNA sequence is encompassed by this invention.

15 Vectors useful for constructing eukaryotic expression systems for the production of recombinant PND comprise the DNA sequence for PND, fragment or variant thereof, operatively linked thereto with appropriate transcriptional activation DNA sequences, such as a promoter and/or operator. Other typical features 20 may include appropriate ribosome binding sites, termination codons, enhancers, terminators, or replicon elements. These additional features can be inserted into the vector at the appropriate site or sites by conventional splicing techniques such as restriction endonuclease digestion and ligation.

25 Yeast expression systems, which are one variety of recombinant eukaryotic expression systems, generally employ *Saccharomyces cerevisiae* as the species of choice for expressing recombinant proteins. *S. cerevisiae* and similar yeasts possess well known promoters useful in the construction of yeast expression systems, including but not limited to *GAP491*, *GAL10*, *ADH2*, and alpha mating factor.

30 Yeast vectors useful for constructing recombinant yeast expression systems for expressing PND include, but are not limited to, shuttle vectors, cosmid plasmids, chimeric plasmids, and those having sequences derived from 2-micron circle plasmids.

35 Insertion of the appropriate DNA sequence coding for PND, fragment or variant thereof, into these vectors will, in principle, result in a useful recombinant yeast expression system for PND where the modified vector is inserted into the appropriate host cell, by transformation or other means.

40 Recombinant mammalian expression systems are another means of producing the recombinant PND for the conjugates of this invention. In general, a host mammalian cell can be any cell that has been efficiently cloned in cell culture. Host mammalian cells useful for the purposes of constructing a recombinant mammalian expression system include, but are not limited to, Vero cells, NIH3T3, GH3, COS, murine C127 or mouse L cells. Mammalian expression vectors can be based on virus vectors, plasmid vectors which may have SV40, BPV or other viral replicons, or vectors without a replicon for animal cells. Detailed discussions on mammalian expression vectors can be found in the treatises of Glover, D.M. (ed.) "DNA Cloning: A Practical Approach," IRL 1985, Vols. I and II.

45 Recombinant PND may possess additional and desirable structural modifications not shared with the same organically synthesized peptide, such as adenylation, carboxylation, glycosylation, hydroxylation, methylation, phosphorylation or myristylation. These added features may be chosen or preferred as the case may be, by the appropriate choice of recombinant expression system. On the other hand, recombinant PND may have its sequence extended by the principles and practice of organic synthesis of section A above.

Conjugation of PND and Omp to Form a Covalent Linkage(s) Yielding Conjugate

50 Antigenic conjugates of PND and Omp are useful for vaccination against AIDS or ARC. Such conjugates have at least one covalent linkage between the antigen PND and Omp, and typically have more than one PND molecule covalently bound to each Omp molecule.

55 PND and Omp are prepared separately, then linked by non-specific cross-linking agents, monogeneric spaces or bigeneric spacers. Methods for non-specific cross-linking include, but are not limited to, reaction with glutaraldehyde; reaction with N-ethyl-N'-(3-dimethylaminopropyl) carbodiimide, with or without admixture of a succinylated carrier; periodate oxidation of glycosylated substituents followed by coupling to free amino groups of a protein carrier in the presence of sodium borohydride or sodium cyanoborohydride; diazotization of aromatic amino groups followed by coupling on tyrosine side chain residues of the protein;

reaction with isocyanates; or reaction of mixed anhydrides. See, generally, Briand, J.P. et al. *J. Imm. Meth.* 78, 59 (1985). These methods of non-specifically cross-linking are conventional and well-known in the typical practice of preparing conjugates for immunological purposes.

In another embodiment of the invention conjugates formed with a monogeneric spacer are prepared.

- 5 These spacers are bifunctional and require functionalization of only one of the partners of the reaction pair to be conjugated before conjugation takes place.

By way of illustration rather than limitation, an example of a monogeneric spacer involves coupling the polypeptide PND to one end of the bifunctional molecule adipic acid dihydrazide in the presence of carbodiimide. A diacylated hydrazine presumably forms with pendant glutamic or aspartic carboxyl groups of PND. Conjugation then is performed by a second coupling reaction with carrier protein in the presence of carbodiimide. For similar procedures, see for example, Schneerson, R. et al., *J. Exp. Med.* 152, 361 (1980). Another example of a monogeneric spacer is described in Fujii, N. et al. *Int. J. Peptide Protein Res.* 26, 121 (1985).

In another embodiment of the invention conjugates of PND and Omp are formed with a bigeneric spacer. These spacers are formed after each partner of the reaction pair to be conjugated, e.g., PND and Omp, is functionalized with a bifunctional spacer. Conjugation occurs when each functionalized partner is reacted with its opposite partner to form a stable covalent bond or bonds. See, for example, Marburg, S. et al., *J. Am. Chem. Soc.* 108, 5282-5287 (1986) and Marburg, S. et al., U.S. Patent 4,695,624, issued September 1987, each incorporated by reference. Bigeneric spacers are preferred for preparing conjugates in human vaccines since the conjugation reaction is well characterized and easily controlled.

Typical and conventional immunological practice provides for the ready and easy synthesis of antigenic conjugates within the scope of the present invention, including the conjugation of Omp with virtually any desired degree of substitution of virtually any peptide of the Sequence Listing. Heterogeneous products of the conjugation reaction are easily separable if needed by a variety of suitable column chromatography techniques.

Vaccine Formulation

The form of the immunogen within the vaccine takes various molecular configurations. A single molecular species of the antigenic conjugate $(PND)_n-Omp$ will often suffice as a useful and suitable antigen for the prevention or treatment of AIDS or ARC. Other antigens in the form of cocktails are also advantageous, and consist of a mixture of conjugates that differ by, for example, the degree of substitution (*n*) or the amino acid sequence of PND or both.

An immunological vector or adjuvant may be added as an immunological vehicle according to conventional immunological testing or practice.

The conjugates of this invention when used as a vaccine, are to be administered in immunologically effective amounts. Dosages of between 1 μ g and 500 μ g of conjugate, and preferably between 50 μ g and 300 μ g of conjugate are to be administered to a mammal to induce anti-peptide, anti-HIV, or HIV-neutralizing immune responses. About two weeks after the initial administration, a booster dose may be administered, and then again whenever serum antibody titers diminish. The conjugate should be given intramuscularly at a concentration of between 10 μ g/ml and 1 mg/ml, and preferably between 50 and 500 μ g/ml, in a volume sufficient to make up the total required for immunological efficacy.

Adjuvants may or may not be added during the preparation of the vaccines of this invention. Alum is the typical and preferred adjuvant in human vaccines, especially in the form of a thixotropic, viscous, and homogeneous aluminum hydroxide gel. For example, one embodiment of the present invention is the prophylactic vaccination of patients with a suspension of alum adjuvant as vehicle and a cocktail of $(PND)_n-Omp$ as the selected set of immunogens or antigens.

The vaccines of this invention may be effectively administered, whether at periods of pre-exposure and/or post-exposure, in combination with effective amounts of the AIDS antivirals, immunomodulators, anti-infectives, or vaccines of Table I.

TABLE IANTI-VIRALS

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
AL-721	Ethigen (Los Angeles, CA)	ARC, PGL HIV positive, AIDS
Recombinant Human Interferon Beta	Triton Biosciences (Almeda, CA)	AIDS, Kaposi's sarcoma, ARC
Acemannan	Carrington Labs (Irving, TX)	ARC (See also immuno-modulators)
Cytovene Ganciclovir	Syntex (Palo Alto, CA)	sight threatening CMV peripheral CMV retinitis
d4T Didehydrodeoxy-thymidine	Bristol-Myers (New York, NY)	AIDS, ARC
dd Dideoxyinosine	Bristol-Myers (New York, NY)	AIDS, ARC
EL10	Elan Corp, PLC (Gainesville, GA)	HIV infection (See also immuno-modulators)
Foscarnet Trisodium Phosphonoformate	Astra Pharm. Products, Inc. (Westborough, MA)	CMV retinitis, HIV infection, other CMV infections

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>	
Dideoxycytidine; ddc	Hoffman-La Roche (Nutley, NJ)	AIDS, ARC	
5			
Novapren	Novaferon Labs, Inc.	HIV inhibitor	
10	(Akron, OH)		
	Diapren, Inc.		
	(Roseville, MN, marketer)		
15			
Peptide T	Peninsula Labs	AIDS	
Octapeptide	(Belmont, CA)		
Sequence			
20			
Retrovir	Burroughs Wellcome	AIDS, adv, ARC	
Zidovudine; AZT	(Rsch. Triangle Park, NC)	pediatric AIDS, Kaposi's sarcoma, asymptomatic HIV infection, less severe HIV disease, neurological involve- ment, in combination w/other therapies, post-exposure pro- phylaxis in health care workers	
25			
30			
35			
40	Rifabutin	Adria Laboratories	ARC
	Ansamycin LM 427	(Dublin, OH)	
		Erbamont	
		(Stamford, CT)	
45			

50

55

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
Dextran Sulfate	Ueno Fine Chem. Ind. Ltd. (Osaka, Japan)	AIDS, ARC, HIV positive asymptomatic
5		
Virazole	Viratek/ICN	asymptomatic HIV
10 Ribavirin	(Costa Mesa, CA)	positive, LAS, ARC
Alpha Interferon	Burroughs Wellcome (Rsch. Triangle Park, NC)	Kaposi's sarcoma, HIV in combination w/Retrovir
15		

Immuno-modulators

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
Antibody which neutralizes pH labile alpha aber- rant Interferon in an immuno- adsorption column	Advanced Biotherapy Concepts (Rockville, MD)	AIDS, ARC
20		
AS-101	Wyeth-Ayerst Labs. (Philadelphia, PA)	AIDS
35		
Propirimine	Upjohn (Kalamazoo, MI)	advanced AIDS
40		
Acemannan	Carrington Labs, Inc. (Irving, TX)	AIDS, ARC (See also anti- virals)
45		

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>	
CL246,738	American Cyanamid (Pearl River, NY)	AIDS, Kaposi's sarcoma	
5	Lederle Labs (Wayne, NJ)		
10	EL10	Elan Corp, PLC (Gainesville, GA)	HIV infection (See also anti-virals)
15	Gamma Interferon	Genentech (S. San Francisco, CA)	ARC, in combination w/TNF (tumor necrosis factor)
20	Granulocyte Macrophage Colony Stimulating Factor	Genetics Institute (Cambridge, MA)	AIDS
25		Sandoz (East Hanover, NJ)	
30	Granulocyte Macrophage Colony Stimulating Factor	Hoeschst-Roussel (Somerville, NJ)	AIDS
		Immunex (Seattle, WA)	
35	Granulocyte Macrophage Colony Stimulating Factor	Schering-Plough (Madison, NJ)	AIDS
40			AIDS, in combination w/Retrovir
45	HIV Core Particle Immunostimulant	Rorer (Ft. Washington, PA)	seropositive HIV

	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	IL-2 Interleukin-2	Cetus (Emeryville, CA)	AIDS, in combination w/Retrovir
10	IL-2 Interleukin-2	Hoffman-La Roche (Nutley, NJ)	AIDS, ARC, HIV, in combination w/Retrovir
15	Immune Globulin Intravenous (human)	Cutter Biological (Berkeley, CA)	pediatric AIDS, in combination w/Retrovir
20	IMREG-1	Imreg (New Orleans, LA)	AIDS, Kaposi's sarcoma, ARC, PGL
25	IMREG-2	Imreg (New Orleans, LA)	AIDS, Kaposi's sarcoma, ARC, PGL
30	Imuthiol Diethyl Dithio Carbamate	Merieux Institute (Miami, FL)	AIDS, ARC
35	INTRON A Alpha-2 Interferon	Schering Plough (Madison, NJ)	Kaposi's sarcoma w/Retrovir: AIDS
40	Methionine- Enkephalin MTP-PE	TNI Pharmaceutical (Chicago, IL)	AIDS, ARC
45	Muramyl- Tripeptide	Ciba-Geigy Corp. (Summit, NJ)	Kaposi's sarcoma

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<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5 Granulocyte Colony Stimulating Factor	Amgen (Thousand Oaks, CA)	AIDS, in combination w/Retrovir
10 rCD4 Recombinant Soluble Human CD4	Genentech (S. San Francisco, CA)	AIDS, ARC
15 Recombinant Soluble Human CD4	Biogen (Cambridge, MA)	AIDS, ARC
20 Roferon-A Interferon Alfa 2a	Hoffman-La Roche (Nutley, NJ)	Kaposi's sarcoma AIDS, ARC, in combination w/Retrovir
25 SK&F106528 Soluble T4	Smith, Kline & French HIV infection Laboratories (Philadelphia, PA)	
30 Thymopentin	Immunobiology Research Institute (Annandale, NJ)	HIV infection
35 Tumor Necrosis Factor; TNF	Genentech (S. San Francisco, CA)	ARC, in combina- tion w/gamma Interferon
40 45		

Anti-Infectives

	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	Clindamycin with Primaquine	Upjohn (Kalamazoo, MI)	PCP
10	Diflucan Fluconazole	Pfizer (New York, NY)	cryptococcal meningitis, candidiasis
15	Pastille Nystatin Pastille	Squibb Corp. (Princeton, NJ)	prevention of oral candidiasis
20	Ornidyl Eflornithine	Merrell Dow (Cincinnati, OH)	PCP
25	Pentamidine Isethionate (IM & IV)	LyphoMed (Rosemont, IL)	PCP treatment
30	Piritrexim	Burroughs Wellcome (Rsch. Triangle Park, NC)	PCP treatment
35	Pentamidine isethionate for inhalation	Fisons Corporation (Bedford, MA)	PCP prophylaxis
40	Spiramycin	Phone-Poulenc Pharmaceuticals (Princeton, NJ)	cryptosporidial diarrhea
45			

5 Drug Name Manufacturer Indication
 Intraconazole- Janssen Pharm. histoplasmosis;
 R51211 (Piscataway, NJ) cryptococcal
 meningitis

10 Trimetrexate Warner-Lambert PCP

15 Other

20 Drug Name Manufacturer Indication
 Recombinant Human Ortho Pharm. Corp. severe anemia
 Erythropoietin (Raritan, NJ) assoc. and Retrovir
 therapy

25 Megestrol Acetate Bristol-Myers treatment of
 (New York, NY) anorexia assoc.
 w/AIDS

30 Total Enteral Norwich Eaton diarrhea and
 Pharmaceuticals malabsorption
 (Norwich, NY) related

35 It will be understood that the scope of combinations of the antigenic conjugates of this invention with
 AIDS antivirals, immunomodulators, anti-infectives or vaccines is not limited to the list in the above Table,
 but includes in principle any combination with any pharmaceutical composition useful for the treatment of
 AIDS. The antigenic conjugates as AIDS or HIV vaccines of this invention include vaccines to be used pre-
 or post-exposure to prevent or treat HIV infection or disease, and are capable of producing an immune
 response specific for the immunogen.

40 EXAMPLE 1

45 Isolation of Genomic DNA from Frozen (-20°C) Pellets of Peripheral Blood Lymphocytes

50 Each DNA was prepared respecting the principle that preparation and storage of high molecular weight
 DNA be segregated from all polymerase chain reaction (PCR) amplification experiments.

Reagents

P-K Buffer

5 10 mM Tris Prepare using sterile H₂O in
400 mM NaCl pH 7.4 plastic labware. Sterile filter
2 mM EDTA through a 0.45 µm filter
10 device and aliquot 10 ml into
 15 ml conical tubes. Store at
 -20°C.

15 Proteinase K 1.0mg/ml Dissolve the contents of a bottle
 in sterile H₂O to a final conc.
20 of 1.0 mg/ml. Aliquot 0.3-0.5 ml
 into freezer tubes. Store at
 -20°C.

25 SDS 10% Prepare using sterile H₂O in
 plastic labware. Sterile filter
30 through a 0.45 µm filter device
 and aliquot 2.0 ml into Nalgene
 freezer tubes. Store at -20°C.

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5 **Phenol:Chloroform 50:50** Prepare and aliquot 8.0 ml into
15 ml conical tubes and store at
-20°C in the dark.

10 **RNase A 1.0 mg/ml** Dissolve the contents of a bottle
in sterile H₂O to a final
conc. of 1.0 mg/ml. Aliquot 0.3-
0.5 ml into freezer tubes. Store
at -20°C.

15 **95% and 70% EtOH** Store at -20°C.

20 **Dilution Buffer**
10 mM Tris Prepare using sterile H₂O in
25 mM NaCl pH 8.0 plastic labware. Sterile filter
0.1 mM EDTA through a 0.45 µm filter device
25 and aliquot 10 ml in 15 ml
 conical tubes. Store at 4°C.

- 30 1) Suspend cell pellets of co-cultivated patient peripheral blood lymphocytes in 0.5 ml of P-K Buffer taking care to break up pellet completely.
2) Adjust sample to 100 µg/ml Proteinase K with 1.0 mg/ml stock. Mix well.
3) Adjust sample to 0.5% SDS with 10% stock. Mix well and incubate at 50°C for 16-24 hours.
4) Extract sample with an equal volume of Phenol: Chloroform for 10 minutes @ 21-25°C.
5) Split phases by centrifugation @ 2K for 5 minutes.
6) Remove aqueous and re-extract with an equal vol. of CHCl₃ for 2-5 minutes @ 21-25°C. Split phases as before.
7) Repeat Step 6.
8) Adjust aqueous to 100 µg/ml RNase A with 1.0 mg/ml stock and incubate @ 37°C for 90 minutes.
9) Repeat Steps 4, 5, 6, and 7.
10) Precipitate DNA with the addition of 2.5 vol of cold 95% EtOH.
40 11) Collect DNA for 30 minutes at 10,000 RPM's at 4°C.
12) Remove EtOH and wash pellet once with 70% EtOH. Spin for 2 minutes as 10,000 RPM's.
13) Remove EtOH and dissolve the pellet in 300µl of dilution buffer.

45 **EXAMPLE 2**
PCR Amplification of Genomic DNA from HIV Isolates

Genomic DNA was amplified by the polymerase chain reaction according to Scharf, S.J. et al. *Science* 233, 1076 (1986). A heat resistant *T. aquaticus* DNA polymerase was employed to enhance stability during thermal cycling. See, e.g., Saiki, R. K. et al. *Science* 239, 487 (1988). Excess primer for each strand was used. The primers were
RP.Hpa having the sequence
5'-P-TCT-GTT-AAC-TTC-ACA-GAC-AAT-GCT-AAA-ACC-ATA-ATA-GTA-CAG-CTG-3'; and
RP.Cla having the sequence
55 5'-P-GCA-ATC-GAT-CTG-TTT-TAA-AGT-GTT-ATT-CCA-TTT-TGC-3'
The 5' phosphate was added by chemical methods, according to Horn, T. et al., *Tetrahedron Letters* 27, 4705 (1986).

EXAMPLE 3

Filtration of PCR Amplified Sequences

5 General Considerations:

This filtration step removes free nucleotides and low molecular weight oligonucleotide contaminants which inhibit ligation, according to Sharf, et al. Science, 233, 1076 (1986).

10 1) Dilute up to 100 λ of sample (1-2 μ g DNA/ml) of Example 2 to 400 λ with "buffer" (10 mM Tris-HCl, 25 mM NaCl, 0.1 mM EDTA, all buffered to pH8) and spin in a microcentrifuge for 5 minutes at RT.

N.B. No more than 4 samples can be placed in same rotors at one time. Be sure that the cap of the tube is completely closed or some volume may spray out of the unit. If using a non-dedicated microcentrifuge, spin sample at 2000 x g.

15 2) Remove insert and place in a clean 1.5 ml plastic tube containing a polysulfone filter with a 100,000 dalton molecular weight cut off. Redilute sample to 400 λ with buffer and spin as before.

3) Repeat Step 2.

4a) For Cloning purposes:

Remove sample and rinse membrane gently with 10-20 λ of buffer. Combine the sample and rinse and adjust back to the original volume. Check on agarose gel for yield and purity.

20 4b) For Reamplification purposes:

Remove sample carefully measuring volume. Rinse the membrane gently with additional buffer as above. Adjust back to the original volume (100 λ) and use 5 λ of the sample for reamplification.

EXAMPLE 4

25 Ligation and Cloning of PCR Amplified Sequences

Reagents

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pUC13 SmaI/Bap

A cloning vector
commercially prepared by
Pharmacia, dissolved in 10
mM Tris pH8.0, aliquoted and
stored at -20°C. Its

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sequence and preparation are
described in Vieira, J. et
al., Gene 19, 259 (1982),
incorporated by reference
for these purposes.

5 5X ligation buffer prepared from stocks
 250 mM Tris pH7.8 aliquoted and stored at
 50 mM MgCl₂ -20°C.
 10 100 mM DTT
 15 5.5 mM ATP
 250 mg/ml BSA

20 T₄ DNA Ligase New England Biolabs

SOC media

25 Final
 Concentration

30 Bactotryptone	2%	- To 97 ml distilled
Yeast Extract	0.5%	H ₂ O, add bacto-
NaCl	10 mM	tryptone, yeast
35 KC1	2.5 mM	extract, NaCl and
MgCl ₂ , MgSO ₄	20 mM (10 mM each)	KC1. Stir to dis-
Glucose	20 mM	solve, autoclave,
40 Distilled H ₂ O	-----	and cool to room
		temperature. Make
		medium 20 mM in
		Mg ⁺⁺ stock with
		a 2 M Mg ⁺⁺ (1 M
		MgCl ₂ •6H ₂ O +
		1 M MgSO ₄ •

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5 $7\text{H}_2\text{O}$, filter-
 sterilized). Add
 2^4M glucose
 stock (filter-
 sterilized) to
 make the medium
 20 mM final.
 Filter the
 complete medium
 through a 0.2 -
 μm filter unit.
 pH should be 7.0
 ± 0.1 . Filter-
 sterilizing units
 should be pre-
 filtered with
 distilled H_2O
 before use to
 remove any toxic
 material from the
 filter.

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Luria Bertani Agar + 100 $\mu\text{g}/\text{ml}$

Ampicillin - commercially prepared from
 REMED. For composition, see
 Sambrook, J. et al., Molecular
 Cloning 3, A.1 (2nd Ed., 1989)

Xgal 2% in dimethyl-
 formamide

- stored at -20°C. Xgal is
 5-bromo-4-chloro-3-indolyl
 β -D-galactoside.

IPTG 100 mM in H_2O

- stored at -20°C. IPTG is
 isopropyl-thiogalactoside.

- 55 1). Combine 10 λ of filtered PCR amplified DNA (10-20 ng/ml) with 20 ng of pUC13 SmaI/BAP and 100 units of T₄ DNA ligase in a final volume of 20 λ .
- 2). Incubate at 21-25 °C for 3 hours.
- 3). Transform 100 λ of transformation competent bacteria using 10 λ of ligation buffer.
- 4). Incubate on ice for 30 minutes in sample tubes.

- 5) Heat shock tubes for 45 seconds at 42°C.
- 6) Reincubate on ice for 2 minutes before adding 1.0 ml of SOC media (21-25°C).
- 7) Incubate 1 hour at 37°C shaking at 225 RPM's.
- 8) Pellet cells in 1.5 ml plastic tubes for 10 seconds at maximum speed.
- 9) Remove the media except about 100λ. Care should be taken removing the media as the pellet is loose.
- 10) Resuspend the cells in the remaining 100λ and spread on an L agar plate containing Ampicillin and onto which 100λ of Xgal and 50λ of IPTG had been previously spread.
- 11) Invert the incubate at 37°C. Colonies are visible after 12 hours. Blue color indication is clear after 16 hours.

EXAMPLE 5

Isolation of Plasmid DNA for Subsequent Dideoxy Sequence Analysis

15 Reagents

MP Buffer 1

20 50 mM Glucose
10 mM EDTA
25 mM Tris pH 8.0

MP Buffer 2 - made fresh for each experiment

25 0.2 N NaOH
1% SDS

MP Buffer 3

30 Potassium Acetate pH ~5.6
60 ml 5M KOAc
28.5 ml H₂O
11.5 ml gl. HOAc

35 RNase Stock

1.0 mg/ml RNase A dissolved in H₂O and boiled
10 minutes

40 Phenol:Chloroform (50:50)

Phenol is buffer saturated with an equal volume of buffer (50 mM Tris-HCl, 100 mM NaCl, 1mM EDTA, pH 8.0)

45 PEG

13% Poly Ethylene Glycol (PEG-8000)

50 4M NaCl

95% and 70% EtOH

- 1). Three individual colonies from each isolate are selected at random and placed in 10 ml of L Broth.
Each are grown overnight in a 50 ml conical tube shaking @ 225-250 RPM's @ 37°C.
- 2). Collect 9.5 ml of overnight culture at 1K for 20 minutes.
- 3). Dry pellet well and resuspend by vortexing in 200λ of MP 1. Transfer to a 1.5 ml plastic tube.
Incubate 5 minutes @ RT.

- 4). Add 40 λ of MP 2 and incubate 5 minutes on ice. Mix by inversion.
5). Add 300 λ of MP 3 and incubate 5 minutes on ice. Mix by inversion.
6). Centrifuge 10,000 Xg for 5 minutes @ 4 °C.
7). Transfer supernatant to a fresh 1.5 ml tube and add 10 λ of a 1.0 μ g/ml RNase A stock. Incubate 30 minutes @ 37 °C.
8). Extract with an equal volume (-500 λ) of buffer saturated phenol:chloroform. Split phases.
9). Transfer aqueous to a fresh tube and precipitate by adding 1.0 ml of cold EtOH. Incubate @ -70 °C for 30 minutes.
10). Collect at full speed (about 10,000 Xg) for 15 minutes @ 4 °C.
11). Remove EtOH and wash with 1.0 ml cold 70% EtOH. Respin for 2 minutes.
12). Remove EtOH and drain tube well. Dry pellet by inversion and then redissolve in 80 λ H₂O.
13). Adjust sample with 20 λ 4M NaCl and 100 λ PEG. Incubate 30 minutes on ice.
14). Centrifuge at full speed (about 10,000 Xg) for 15 minutes @ 4 °C.
15). Remove supernatant and wash pellet with 1.0 ml cold 70% EtOH. Respin for 2 minutes.
16). Remove EtOH and drain tube well. Dry pellet in speed vac. and then redissolve in 20 λ H₂O.

EXAMPLE 6

DETERMINATION OF THE DNA SEQUENCE

Sequencing was performed by the method of Tabor, S. et al., Proc. Natl. Acad. Sci., 84, 4767 (1987). Sequencing gels were read and checked with a scanner. Amino acid sequences were deduced from DNA.

EXAMPLE 7

Preparation of Synthetic Peptides

A The oligopeptide EE15-1 of the sequence:

30 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA

35
Arg Arg Ala Tyr Cys
45 AGA CGA GCA TAT TGT

is synthesized by conventional solid-phase techniques on an automated peptide synthesizer, according to Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al.(eds.), *Synthetic Peptides in Biology and Medicine*, Elsevier 1985, pp. 29-57.

B. Each of the peptides of the Sequence Listing is prepared by the same method.

C. Oligopeptide EE15-1 was prepared in a recombinant expression system in *E. coli* according to the methods of Sambrook, J. et al., Molecular Cloning 3, 17.3 et seq. Cold Spring Harbor 2nd Ed. 1988.

Every other peptide of the Sequence Listing is also prepared in a recombinant expression system in *E. coli*.

EXAMPLE 8

Extraction and Purification of Omp**A. First Method**

5 All materials, reagents and equipment were sterilized by filtration, steam autoclave or ethylene oxide, as appropriate; aseptic technique was used throughout.

A 300 gm (wet weight) aliquot of 0.5% phenol inactivated cell paste of Meningococcal group B11 was suspended in 1200 mls of distilled water than suspended by stirring magnetically for 20 minutes at room temperature. The suspended cells were pelleted at 20,000 x g for 45 minutes at 5°C.

10 For extraction, the washed cells were suspended in 1500 mls 0.1 M Tris, 0.01 M EDTA Buffer pH 8.5 with 0.5% sodium deoxycholate (TED Buffer) and homogenized with a 500 ml Sorvall omnimixer at setting 3 for 60 seconds. The resulting suspension was transferred to ten Erlenmeyer flasks (500 ml) for extraction in a shaking water bath for 15 minutes at 56°C. The extract was centrifuged at 20,000 x g for 90 minutes at 5°C and the viscous supernatant fluid was decanted (volume = 1500 mls). The decanted fluid was very 15 turbid and was recentrifuged to clarify further at 20,000 x g for 90 minutes at 5°C. The twice spun supernatant fluid was stored at 5°C. The extracted cell pellets were resuspended in 1500 mls TED Buffer. The suspension was extracted for 15 minutes at 56°C and recentrifuged at 20,000 x g for 90 minutes. The supernatant fluids which contained purified Omp were decanted (volume = 1500 mls) and stored at 5°C.

B. Second Method

All material, reagents, equipment and filters were sterilized by heat, filtration or ethylene oxide. One exception was the K-2 ultracentrifuge which was sanitized with a 0.5% formalin solution. Laminar flow canopies provided sterility protection during equipment connections. Aseptic techniques were followed 25 throughout the entire operations. Overnight storage of the protein was at 2-8°C between steps. A 0.2 micron sterile filtration was conducted just before the final diafiltration to ensure product sterility.

Two 600-liter batches of Neisseria meningitidis were fermented and killed with 0.5% phenol, then concentrated to roughly 25 liters using two 10 ft² 0.2 micron polypropylene cross-flow filtration membranes. The concentrated broth then was diafiltered with 125 liters of cell wash buffer (0.11 M Sodium Chloride, 30 17.6 mM Sodium Phosphate Diabasic, 23.3 mM Ammonium Chloride, 1.34 mM Potassium Chloride, adjusted to pH 7 with 85% Phosphoric Acid followed by 2.03 mM Magnesium Sulfate Heptahydrate).

For extraction, an equal volume of 2X-TED buffer (0.2M Tris, 0.02M EDTA adjusted to pH 8.5 with concentrated HCl followed with the addition of 1.0% sodium deoxycholate) was added to the cell slurry. The resulting slurry was heated to 56 ± 3°C and maintained at this temperature for 30 minutes to complete the 35 extraction of Omp from the cells.

For further purification, the extracted cell slurry was centrifuged at 30,000 x g (18,000 rpm) in a "one-pass" flow mode in a K-ultracentrifuge, and the supernatant stream was collected. The low-speed supernatant was concentrated to 10 liters on two 0.1-micron polysulfone autoclavable hollow-fiber membranes and collected in an 18 liter sterile bottle. The filtration equipment was given two 4-liter rinses with 40 TED buffer (0.1M Tris, 0.01M EDTA, adjusted to pH 8.5 with concentrated HCl, followed with the addition of sodium deoxycholate to 0.5%) which was combined with the retentate. The retentate was subdivided into two or three equal parts. Each part was centrifuged at 80,000 x g (35,000 rpm) for 30 mintues. The Omp 45 protein was pelleted, and the majority of soluble proteins, nucleic acids and endotoxins remained in the supernatant. The supernatant was discarded. The pelleted protein was resuspended by recirculating 55 ± 5°C TED buffer through the rotor. The first high-speed resuspensions were combined and subjected to a second low-speed spin. The second low speed spin ensured that residual cell debris was removed from the product stream. The second low speed supernatant was subdivided into two or three equal parts. Each fraction was given two consecutive high-speed spins. All high-speed spins were operated under the same conditions and each further purified the Omp protein.

50 For sterile filtration and final diafiltration, the third high-speed resuspensions were diluted with an equal volume of TED buffer and filtered through a 0.2 micron cellulose acetate filter. When all fractions were permeated, an 8 L TED buffer rinse was used to flush the filtration system. The permeate and rinse were combined and concentrated to 3 liters on a 0.1 micron polysulfone autoclavable hollow fiber membrane. The material then was diafiltered with 15 liters of sterile pyrogen free water. The retentate was collected in a 4-liter bottle along with a 1-L rinse to give the final product. The final aqueous suspension was stored at 2-8°C, as purified Omp.

C. Third Method

Omp is purified from 0.2 M LiCl-0.1M Na Acetate, pH 5.8, extracts by ultracentrifugation, by the method of C.E. Frasch *et al.* *J. Exp. Med.* **140**, 87-104 (1974), herein incorporated by reference.

EXAMPLE 9

5

A. Preparation of (EE15-1 Peptide)-Omp conjugate ("EE15-1-Omp" conjugate)

N-acetylhomocystaminylated outer membrane protein (Omp) of *N. meningitidis* from 59 mg of Omp (purified by Method B of Example 2) is prepared by the centrifugation method described in Marburg, S. *et al.*, *J. Am. Chem. Soc.* **108**:5282 (1986). This material (about 50 mg) is reacted at pH 8 (6.5 mL 0.1M PO₄ buffer) with 20 mg of N- ω -bromoacetylated EE15-1 (lyophilized) under N₂ for 18 hours at room temperature.

The reaction mixture is diluted to 10 mL with H₂O and centrifuged for 2h, at 4 °C and 43,000 rpm. The supernatant is removed, and the pellet resuspended, using a Dounce tissue homogenizer, in 10 mL of H₂O. This suspension is recentrifuged (as above) and the pellet resuspended in 9.5 mL of H₂O. A low speed spin for 1 minute in a clinical centrifuge removes a flocculent insoluble material if any. The degree of substitution can be determined and calculated by a variety of methods.

B. Preparation of Other Peptide Conjugates

20 By the method of Example 9A the following peptide-Omp conjugates are obtained:

(EE15-1)₅-Omp,
 (EE164-3)₄-Omp,
 (EE244-1)₆-Omp,
 (EE310-2)₈-Omp,
 25 (EE311-1)₁₀-Omp,
 (EE359-2)_{6.5}-Omp,
 (EE360-1)_{3.3}-Omp, and
 (EE543-1)_{4.0}-Omp.

EXAMPLE 10

Protocol for Inoculation of Animals with the (EE15-1)₅-Omp Conjugate (hereinafter "EE-15-1-Omp" conjugate)

35 Alum is used as an adjuvant during the inoculation series. The inoculum is prepared by dissolving the EE15-1-Omp conjugate in physiologic saline at a final conjugate concentration of 100 µg/ml. Preformed alum (aluminum hydroxide gel) is added to the solution to a final level of 500 µg/ml aluminum. The conjugate is allowed to adsorb onto the alum gel for two hours at room temperature. Following adsorption, the gel with the conjugate is washed twice with physiologic saline and resuspended in the saline to a protein concentration of about 100 µg/ml.

40 African green monkeys are individually inoculated with four 100 mcg doses of the EE15-1-Omp conjugate adsorbed onto alum. Each dose is injected intramuscularly. The doses are delivered one or five months apart (week 0, 4, 8 and 28). The animals are bled at intervals of two or four weeks. Serum samples are prepared from each bleed to assay for the development of specific antibodies as described in the subsequent examples.

EXAMPLE 11

Analysis of Sera for Anti-Peptide IgG Antibodies

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Each serum sample is analyzed by enzyme-linked immunoassay (ELISA). Polystyrene microtiter plates are coated with 0.5 µg per well of the synthetic peptide (not conjugated to Omp) in phosphate-buffered physiological saline (PBS) at 4 °C. Each well is then washed with PBS containing 0.05% TWEEN-20 (PBS-T). Test serum, diluted serially in PBS-T, is added to the peptide-containing wells and allowed to react with the adsorbed peptide for one hour at 36 °C. After washing with PBS-T, alkaline phosphatase-conjugated goat anti-human IgG is added to the test wells and is allowed to react for one hour at 36 °C. The wells are then washed extensively in PBS-T. Each well receives 0.1% p-nitrophenyl phosphate in 10% diethanolamine, pH 9.8, containing 0.5 mM MgCl₂H₂O. The ensuing reaction is allowed

to proceed at room temperature for 30 minutes, at which time it is terminated by the addition of 3.0 N NaOH.

- The greater the interaction of antibodies in the test serum with the peptide substrate, the greater is the amount of alkaline phosphatase bound onto the well. The phosphatase enzyme mediates the breakdown of p-nitrophenyl phosphate into a molecular substance which absorbs light at a wavelength of 405 nm. Hence, there exists a direct relationship between the absorbance at 405 nm of light at the end of the ELISA reaction and the amount of peptide-bound antibody.
- 5 Titters of anti-(EE15-1-Omp) antibody are thus readily determined.

10 **EXAMPLE 12**

Analysis of Sera for Activity which Specifically Neutralizes HIV Infectivity

Virus-neutralizing activity is determined with an assay described by Robertson et al., J. Virol. Methods 20: 195-202 (1988). The assay measures specific HIV-neutralizing activity in test serum. The assay is based 15 on the observation that MT-4 cells, a human T-lymphoid cell line, are readily susceptible to infection with HIV and, after a period of virus replication, are killed as a result of the infection.

The test serum is treated at 56°C for 60 minutes prior to the assay. This treatment is required to 20 eliminate non-specific inhibitors of HIV replication. Heat treated serum, serially diluted in RPMI-1640 cell culture medium, is mixed with a standard infection dose of HIV. The dose is determined prior to the assay as containing the smallest quantity of virus required to kill all the MT-4 cells in the assay culture after a period of 7 days. The serum-virus mixture is allowed to interact for one hour at 37°C. It then is added to 1.0 x 10⁵ MT-4 cells suspended in RPMI-1640 growth medium supplemented with 10% fetal bovine serum. The cultures are incubated at 37°C in a 5% CO₂ atmosphere for 7 days.

25 At the end of the incubation period, a metabolic dye, DTT, is added to each culture. This dye is yellow in color upon visual inspection. In the presence of live cells, the dye is metabolically processed to a molecular species which yields a blue visual color. Neutralized HIV cannot replicate in the target MT-4 cells and therefore does not kill the cells. Hence, positive neutralization is assessed by the development of blue color following addition of the metabolic dye.

30 All the monkeys inoculated with the EE15-1-Omp conjugate are bled for specific HIV infectivity-neutralizing activity. Further follow-up evaluation of the same monkeys is also performed. Booster shots are also administered to ascertain renewed neutralizing titer.

While the foregoing specification teaches the principles of the present invention, with examples provided for the purpose of illustration, it will be understood that the practice of the invention encompasses 35 all of the usual variations, adaptations, modifications, deletions or additions of procedures and protocols described herein, as come within the scope of the following claims and its equivalents.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: J.A. LEWIS ET AL.
- (ii) TITLE OF INVENTION: NEW EMBODIMENTS OF THE
HIV PRINCIPAL NEUTRALIZING DETERMINANT
- (iii) CORRESPONDENCE ADDRESS: MERCK & CO., INC.
 - (A) STREET: P.O. BOX 2000, EAST LINCOLN AVE.
 - (B) CITY: RABWAY
 - (C) STATE: NEW JERSEY
 - (D) COUNTRY: USA
 - (E) ZIP: 07065
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 5.25 in., 360 Kb storage
 - (B) COMPUTER: Wang PC 381
 - (C) OPERATING SYSTEM: MS-DOS 3.30.10
 - (D) SOFTWARE: Microsoft WORD 5.0
- (v) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: NA
 - (B) FILING DATE: NA
 - (C) CLASSIFICATION: NA
- (vi) PRIOR APPLICATION DATA: NONE
 - (A) DOCUMENT NUMBER: _____
 - (B) COUNTRY: _____
 - (C) FILING DATE: _____
 - (D) PUBLICATION DATE: _____
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: R.D. MEREDITH
 - (B) REGISTRATION NUMBER: 30,777
 - (C) REFERENCE/DOCKET NUMBER: 18114Y
- (viii) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-594-4678
 - (B) TELEFAX: 201-594-4720
 - (C) TELEX: _____
- (ix) PUBLICATION STATUS: NOT KNOWN
 - (A) AUTHORS: _____
 - (B) TITLE: _____
 - (C) JOURNAL: _____
 - (D) VOLUME: _____
 - (E) ISSUE: _____
 - (F) PAGES: _____
 - (G) DATE: _____
 - (H) RELEVANT RESIDUES:
 - (1) START: _____
 - (2) END: _____
 - (3) BASE PAIRS: _____
 - (4) AMINO ACIDS: _____

(2) INFORMATION FOR SEQ ID NO: EE15-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND:cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL
ISOLATE: _____

(vi) IMMEDIATE SOURCE:

(vii) CLONE: _____

(viii) POSITION IN GENOME: Within Env Gene

(ix) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE15-1

1	5	10	15											
Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Arg	Gly	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AGC	AAC	AAT	ACA	AGA	AGA	GGT	ATA	CAT	ATA	GGA

20	25	30												
Pro	Gly	Arg	Ala	Leu	Tyr	Thr	Thr	Gly	Glu	Ile	Thr	Gly	Asp	Ile
CCA	GGG	AGA	GCA	CTT	TAT	ACA	ACA	GCA	GAA	ATA	ACA	GGA	GAT	ATA

35				
Arg	Arg	Ala	Tyr	Cys
AGA	CGA	GCA	TAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE15-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND:cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 5 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 10 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE15-2

1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly
 TGT ACA AGG CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

20

20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCC TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

25

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

30

(2) INFORMATION FOR SEQ ID NO: EE15-3

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 35 (ii) KIND: cDNA to genomic RNA
 (iii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 40 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 45 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____

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- (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION: SEQ ID NO: ____

5

SEQ ID NO: EE15-3

10 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly
 TGT ACA AGG CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

15 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCC TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

20 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 25 (2) INFORMATION FOR SEQ ID NO: EEE37-1
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 30 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 35 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 40 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

45

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55

SEQ ID NO: EEE37-1

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Thr MET Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGG ATA ACT ATG GGA

10 20 25 30
 Pro Gly Arg Val Phe Tyr Thr Thr Gly Gly Ile Ile Gly Asn Ile
 CCA CGG AGA GTA TTT TAT ACA ACA GGA GGA ATA ATA GGA AAT ATA

15 35
 Arg Arg Ala His Cys
 AGA CGA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EEE37-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 25 (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 30 (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- 35 (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EEE37-2

1 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 45 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile	CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA	

35

(2) INFORMATION FOR SEQ ID NO: EE37-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: I

(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE:

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic

determinant

SEQ. ID. NO.: EE37-3

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Asn	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	AAT	ATA	GGA

20	25	30
Pro Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Gly Asp		
CCA GGA CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA GGA GAT		

35

- (2) INFORMATION FOR SEQ ID NO: EE54-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE: _____
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE54-1

25 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATC AAT ATA CGA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ATA GGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EEE69-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

50

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- 5 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 10 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 15 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 20 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

25 SEQ ID NO: EEE69-1

1 5 10 15
 Cys Thr Arg Leu Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 20 TGT ACA AGG CTC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 25 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

30 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 35 (2) INFORMATION FOR SEQ ID NO: EEE69-2
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 40 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 45 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 50 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE69-2

5 1 5 10 15
 Cys Thr Arg Leu Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CTC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala Gln Cys
 AGA CAA GCA CAG TGT

(2) INFORMATION FOR SEQ ID NO: EE74-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE74-1

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

50

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20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA CGA GAT ATA

5 35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 10 (2) INFORMATION FOR SEQ ID NO: EE74-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 15 (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 20 (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- 25 (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30 SEQ ID NO: EE74-2

35 1 5 10 15

Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

40 20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACC ACA GGA GAC ATA ATA GGA GAT ATA

45 35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE74-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vi) POSITION IN GENOME: Within Env Gene
- (vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE74-3

25 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EEE90-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

15 SEO ID NO: EEE90-1

	1	5	10	15
20	Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Ala	TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA		

	20					25					30				
25	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAC	GCA	ACA	GGA	GAA	ATA	ATA	CGA	GAT	ATA

35

- 35 (2) INFORMATION FOR SEQ ID NO: EE90-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40 (ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

45 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

50 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE90-2

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 20 (2) INFORMATION FOR SEQ ID NO: EE90-3
- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - 25 (ii) KIND: cDNA to genomic RNA
 - 25 (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
 - 30 (iii) ORIGINAL SOURCE: HIV
 - 30 (iii) (E) INDIVIDUAL ISOLATE: _____
 - 30 (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
 - 35 (v) POSITION IN GENOME: Within Env Gene
 - 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - 35 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE90-3

45 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

50

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	20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile	CCA GGG AGA GCA TTT TAC CCA ACA GGA GAA ATA ATA GGA GAT ATA		

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10
(2) INFORMATION FOR SEQ ID NO: EE100-1

15
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20
(ii) KIND: cDNA to genomic RNA
(ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

25
(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____
(iv) IMMEDIATE SOURCE:
(C) CLONE: _____
(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE100-1

1 5 10 15
Cys Thr Arg Pro His Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGC ACA AGA CCC CAC AAC AAT ACA AGG AAA AGT ATA CAT ATA GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EEE100-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE100-2

25 1 5 10 15
 Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGC ACA AGA CCC GGC AAC AAT ACA AGG AAA AGT ATA CAT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA CGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE100-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

15 SEQ ID NO: EE100-3

1	5	10	15
20	Cys Thr Arg Pro His Asn Asn Thr Arg Lys Ser Ile His Ile Gly	TGC ACA AGA CCC CAC AAC AAT ACA AGG AAA AGT ATA CAT ATA GGA	

1	5	10	15
25	Pro Gly Arg Ala Trp Tyr Thr Thr Gly Ala Ile Ile Gly Asp Ile	CCA GGG AGA GCA TGG TAT ACA ACA GGA GCA ATA ATA CGA GAT ATA	

35

- 35 (2) INFORMATION FOR SEQ ID NO: EE125-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) KIND: cDNA to genomic RNA
(iii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

45 (iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

50 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE125-1

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Leu Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT CTA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE125-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 25 (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 30 (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- 35 (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE125-2

1 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Leu Gly
 45 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT CTA GGA

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20 25 30

Pro Gly Lys Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGA AAA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

5

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Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

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(2) INFORMATION FOR SEQ ID NO: EEE125-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):

20

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

25

- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____

30

- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene

- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE125-3

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Leu Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT CTA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE131-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE131-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Ser	Lys	Arg	Ile	Ser	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGC	AAA	AGA	ATA	TCT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Arg	Ala	Thr	Arg	Ile	Ile	Gly	Asp	Ile	Arg
	CCA	GGG	AGA	GCT	TTT	CGT	GCA	ACA	AGA	ATA	ATA	GGA	GAT	ATA	AGA

35	35			
	Gln	Ala	His	Cys
	CAA	GCA	CAT	TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE131-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment

(iii) (C) HYPOTHETICAL: _____
ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE131-2

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Ser Lys Arg Ile Ser Ile Gly	TGT ACA AGA CCC AAC AAC AAT ACA AGT AAA AGA ATA TCT ATA GGA		

20	25	30
Pro Gly MET Ala Phe Arg Ala Thr Arg Ile Ile Gly Asp Ile Arg		
CCA CGG ATG GCA TTT CGT GCA ACA AGA ATA ATA GGA GAT ATA AGA		

25 Gln Ala His Cys
CAA GCA CAT TGT 35

30 (2) INFORMATION FOR SEQ ID NO: EE131-3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35 (ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

40 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

45 (v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE131-3

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Ser Lys Arg Ile Ser Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGC AAA AGA ATA TCT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Arg Ala Thr Arg Ile Ile Gly Asp Ile Arg
 CCA GGG AGA GCA TTT CGT GCA ACA AGA ATA ATA GGA GAT ATA AGA

15 35
 Gln Ala His Cys
 CAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EEE149-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EEE149-1

45 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

20 25 30

Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE149-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE149-2

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

50

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

55

- (2) INFORMATION FOR SEQ ID NO: EE149-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE149-3

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Gly	Ile	Ser	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AGG	GGT	ATA	AGT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Val	Tyr	Ala	Thr	Lys	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	GTT	TAT	GCA	ACA	AAA	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EEE159-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment

- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE159-1

1	5	10	15											
Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AGC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EEE159-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL ISOLATE: _____

(vi) IMMEDIATE SOURCE:

(vii) CLONE: _____

(viii) POSITION IN GENOME: Within Env Gene

(ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(x) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE159-2

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA CCT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE159-3

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 25 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 30 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 35 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic
 determinant
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE159-3

1 1 5 10 15
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
 45 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly

50 20 25 30
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile

35
 AGA CAA GCA CAT TGT
 Arg Gln Ala His Cys

- 5
- (2) INFORMATION FOR SEQ ID NO: EE164-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 10 (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 15 (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- 20 (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:
- 25

SEQ ID NO: EE164-1

30 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Ser Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGC AAA GGT ATA CAT ATA GGA

35 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asn Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA AAT ATA ATA GGA AAT ATA

40 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 45 (2) INFORMATION FOR SEQ ID NO: EE164-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
- 50

- 5
- (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA
 - (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
 - (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
 - (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
 - (v) POSITION IN GENOME: Within Env Gene
 - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - (viii) SEQUENCE DESCRIPTION:
- 10
- 15

SEQ ID NO: EEE164-2

20

1	5	10	15
Cys	Thr Arg Pro Asn Asn Asn	Thr Ser Arg Gly Ile His Ile Gly	
TGT	ACA AGA CCC AAC AAC	AAT ACA AGC AGA GGT	ATA CAT ATA GGA

25

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asn Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT GCA ACA GGA AAT ATA ATA GGA GAT ATA		

30

35		
Arg Arg Ala His Cys		
AGA CGA GCA CAT TGT		

35

- (2) INFORMATION FOR SEQ ID NO: EEE164-3
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA
 - (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

50

55

- 5
 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

10

SEQ ID NO: EEE164-3

15
 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA

25 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 30 (2) INFORMATION FOR SEQ ID NO: EE179-1
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 35 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 40 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 45 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

50

55

SEQ ID NO: EE179-1

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAC TGT

20 (2) INFORMATION FOR SEQ ID NO: EE179-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (vi) POSITION IN GENOME: Within Env Gene
- (vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE179-2

45 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

50

55

	20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile	CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA		

5

35

10

(2) INFORMATION FOR SEQ ID NO: EE179-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL:

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE:

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES

determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE179-3

35

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

40

20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

45

Arg Gln Ala His Cys
AGA CAA GCA CAC TGT

50

- (2) INFORMATION FOR SEQ ID NO: EEE181-1
- 1 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 5 (ii) KIND: cDNA to genomic RNA
- 10 (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 15 (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- 20 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE181-1

25 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACC GGA GAA ATA ATA GGA AAT ATA

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE181-2
- 41 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 45 (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE181-2

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA CGA

20 25 30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
CCA GGG AGA GCA TTT TAT ACA ACG GGA GAA ATA ATA GGA AAT ATA

35

- (2) INFORMATION FOR SEQ ID NO: EE181-3

(i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE181-3

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA ACT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gly Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACG GGA GGA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE211-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25 (ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

30 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

35 (v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic
determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE211-1

1 5 10 15
 Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly
 45 TGT ACA AGA CCC AAC GAC AAT ACA AGA AGT ATA AAT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAA ATA ATA GGA AAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EEE211-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EEE211-2

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Ser Leu Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA TCT CTA GGA

40

20 25 30

Pro Gly Ser Ala Ile Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGT GCA ATT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

- (2) INFORMATION FOR SEQ ID NO: EE215-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE215-1

25 1 5 10 15
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCG CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE215-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

15 SEQ ID NO: EE215-2

1	5	10	15
20	Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly	TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA	

	20					25					30				
25	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	CCA	TTT	TAT	ACA	ACA	GGA	GAT	ATA	ATA	GGA	GAT	ATA

35

30 Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

- 35 (2) INFORMATION FOR SEQ ID NO: EE215-3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40 (ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

45 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

50 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE215-3

5 1 5 10 15
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EEE217-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EEE217-1

45 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA CGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE217-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

- (ii) KIND: cDNA to genomic RNA

20

- (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment

25

- (C) HYPOTHETICAL: _____

- (iii) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

- (iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene

- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

30

- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE217-2

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

(2) INFORMATION FOR SEQ ID NO: EE228-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE228-1

1	5	10	15
Cys	Thr	Arg	Pro
TGT	ACA	AGA	CCC
			AAC
			AAT
			ACA
			AGA
			AAA
			AGT
			ATA
			CCT
			ATA
			GGA

20	25	30												
Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile
CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAT	ATA	ATA	GGA	GAT	ATA

35				
Arg	Gln	Ala	His	Cys
AGA	CAA	GCA	CAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE228-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE228-2

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly
TCT	ACA	ACA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCA GGG AGA CCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE228-3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE228-3

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE229-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE229-1

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AGA AGT ATA CAT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg
 CCA GGG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA

5

35

Gln Ala His Cys
 CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE229-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

20

(iii) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

25

(iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

30

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE229-2

35

1 5 10 15

Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg
 CCA GGG AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA

45

35

Gln Ala His Cys
 CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE229-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE229-3

25 1 5 10 15
 Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg
 CCA GGG AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA

35
 Gln Ala His Cys
 CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EEE244-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

15 SEO ID NO: EE244-1

1	5	10	15
20	Cys Thr Arg Pro Asn Asn Ile Lys Ile Arg Ser Ile His Ile	TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA	

20	25	30
25 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg		
GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA		

30 Gln Ala Tyr Cys
CAA GCA TAT TGT

- 35 (2) INFORMATION FOR SEQ ID NO: EE244-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) KIND: cDNA to genomic RNA
(iii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

45 (iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE244-2

5 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Ile Lys Ile Arg Ser Ile His Ile
 TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

10 20 25 30
 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg
 GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

15 35
 Gln Ala Tyr Cys
 CAA GCA TAT TGT

(2) INFORMATION FOR SEQ ID NO: EE244-3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE244-3

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Ile Lys Ile Arg Ser Ile His Ile
 TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

20 25 30

Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg
 GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

5

35

Gln Ala Tyr Cys
 CAA GCA TAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE289-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____

- (iv) IMMEDIATE SOURCE: _____

- (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene

- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

- (viii) SEQUENCE DESCRIPTION: _____

30

SEQ ID NO: EE289-1

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACT ACA GGA GAA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

(2) INFORMATION FOR SEQ ID NO: EE289-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE289-2

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
CCA GGG AGA GCA TTT TAT ACT ACA GGA GAA ATA ATA GGA GAT ATA

35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE290-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

15 SEQ ID NO: EE290-1

1	5	10	15
20	Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Leu Gly	TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA CGG	

20	25	30
25 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile	CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA	

35

30 Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

- 35 (2) INFORMATION FOR SEQ ID NO: EE293-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40 (ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

45 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

50 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE293-1

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE293-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) IMMEDIATE SOURCE:
 - (E) INDIVIDUAL ISOLATE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE293-2

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE293-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE293-3

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE295-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE: _____
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE295-1

25 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Lys Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA AAA GAC ATA ATA CGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE295-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 5 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 10 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE295-2

20 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

25 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Lys Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA AAA GAC ATA ATA CGA GAT ATA

30 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE297-1
- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 40 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 45 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 50 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE297-1

5 1 5 10 15
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE297-2

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 25 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 30 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 35 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic
 determinant
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE297-2

1 1 5 10 15
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 45 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE297-3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE297-3

35

1 5 10 15

Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
 TGT ATA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA AAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

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Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

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(2) INFORMATION FOR SEQ ID NO: EE304-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE304-1

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Asn	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGG	AAA	AGT	ATA	AAT	ATA	GGA

20	25	30												
Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

35				
Arg	Gln	Ala	His	Cys
AGA	CAA	GCA	CAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE304-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE304-2

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AGA AGT ATA AAT ATA CGA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile		
CCA CCC ACA CCA TTT TAT ACA ACA GGA GAA ATA ATA CGA GAT ATA		

35

(2) INFORMATION FOR SEQ ID NO: EE304-3

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE304-3

5 1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGG AGA AGT ATA AAT ATA GGA

10 20 25 30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

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(2) INFORMATION FOR SEQ ID NO: EE308-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL
ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE308-1

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
CCA CGC AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE308-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
 - (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
 - (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
 - (v) POSITION IN GENOME: Within Env Gene
 - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE308-2

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

20	25	30
Pro Gly Arg Pro Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile		
CCA GGC AGA CCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA		

35

(2) INFORMATION FOR SEQ ID NO: EE310-1

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

 - (E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

 - (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE310-1

1 5 10 15
 5 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACC AGA AGA GGT ATA CAT ATA GGA

20 25 30
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

15 35
 15 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE310-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE310-2

1 5 10 15
 45 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA GGT ATA CAT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

5 35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10 (2) INFORMATION FOR SEQ ID NO: EE310-3

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 20 (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 25 (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- 30 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE310-3

35 1 5 10 15

Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

40 20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

45 35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE311-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE311-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	His	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACC	AGA	AGA	AGT	ATA	CAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Ala	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GCT	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Arg	Ala	Tyr	Cys
	AGA	CGA	GCA	TAT	TGT

40 (2) INFORMATION FOR SEQ ID NO: EE312-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE312-1

1	5	10	15
Cys	Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly		
TGT	ACA AGG CCC AAC AAC AAT ACA AGA AAA AGT ATA ACT ATA CGA		

20	25	30
Pro Glu Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg		
CCA GAG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA		

Gln Ala His Cys
GAA GCA GAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE312-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE312-2

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg
 CCA GGG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA

15 35
 Gln Ala His
 CAA GCA CAT

(2) INFORMATION FOR SEQ ID NO: EE313-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE313-1

1 5 10 15
 Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly
 TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

50

55

20 25 30

Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile
 CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA

5

35

Arg Arg Ala His Cys
 AGA CGA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE317-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE317-1

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

45

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Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE320-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE320-1

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

20	25	30												
Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

35				
Arg	Gln	Ala	His	Cys
AGA	CAA	GCA	CAT	TGC

- 2) INFORMATION FOR SEQ ID NO: EE320-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 5 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 10 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE320-2

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

20	25	30												
Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
CCA	GGC	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

30	35			
Arg	Gln	Ala	His	Cys
AGA	CAA	GCA	CAT	TGT

- (2) INFORMATION FOR SEQ ID NO: EE322-1
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 35 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 40 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE322-1

5 1 5 10 15
 Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro
 ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA CCA

10 20 25 30
 Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg Gln
 GGG AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA CAA

15 35
 Ala His Cys
 GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE322-2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____

- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE322-2

45 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA CGA GAA ATA ATA CGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE322-3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) IMMEDIATE SOURCE:
 - (E) INDIVIDUAL ISOLATE: _____
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE322-3

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA CGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA CGA GAA ATA ATA CGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE324-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vi) POSITION IN GENOME: Within Env Gene
- (vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE324-1

25	1	5	10	15												
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Asn	Thr	Ile	Lys	Ser	Ile	His	MET	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	ATA	AAA	AGT	ATA	CAT	ATG	GGA	

30	20	25	30												
	Leu	Gly	Arg	Thr	Phe	Tyr	Thr	Thr	Gly	Glu	Val	Ile	Gly	Asp	Ile
	CTA	GGG	AGG	ACA	TTT	TAT	ACA	ACA	GGA	GAA	GTA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE324-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE324-2

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Leu	Gly
TCT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	CTA	GGG

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA CGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE327-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE327-1

1 5 10 15
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE327-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE327-2

1 5 10 15
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Tyr
 AGA CAA GCA CAT TAT

10

(2) INFORMATION FOR SEQ ID NO: EE327-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

(v) IMMEDIATE SOURCE:

- (C) CLONE: _____

(vi) POSITION IN GENOME: Within Env Gene

(vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE327-3

35 1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

(2) INFORMATION FOR SEQ ID NO: EE345-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly
	TGT	ACA	AGA	CCC	AGC	AAT	AAT	ACA	AGA	AAA	GGT	ATA	CAT	ATA	GGG

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Thr	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACG	GGA	GAG	ATA	ACA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE345-2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-2

1	5	10	15
Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly	TGT ACA AGA CCC AGC AAT AAT ACA AGA AAA GGT ATA CAT ATA GGG		

20	25	30
Pro Gly Arg Ala Phe Phe Thr Thr Gly Glu Ile Thr Gly Asp Ile		
CCA GGG AGA GCA TTT TTT ACA ACA GGA GAA ATA ACA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE345-3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-3

1 5 10 15
 5 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AGC AAT ACA AGA AAA AGT ATA CAT ATA GGG

20 25 30
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACG GGA GAG ATA ACA GGA GAT ATA

35
 15 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE356-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE356-1

1 5 10 15
 45 Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ATA AGA CCC AGC AAC ACA AGA AAA AGT ATA ACT ATA GGA

50

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20 25 30

Pro Gly Arg Ala Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE356-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE356-2

35 5 10 15

Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ATA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE356-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE356-3

25 1 5 10 15
 Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ATA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

30 20 25 30
 Pro Gly Arg Ala Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE359-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE359-1

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Asn	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	AAT	ATA	GGG

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile		
CGA CCC ACA CGC TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE359-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL ISOLATE: _____

(vi) IMMEDIATE SOURCE:

(vii) CLONE: _____

(viii) POSITION IN GENOME: Within Env Gene

(ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE359-2

5 1 5 10 15
 Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AAC GAC AAT ACA AGA AGT ATA AAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE359-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE359-3

1 5 10 15
 Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly
 TGT ACA AGA CCC AAC GAC AAT ACA AGA AGT ATA AAT ATA GGA

50

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20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE360-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE360-1

35

1 5 10 15

Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile
 CCA GGG AGA GCC TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

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- (2) INFORMATION FOR SEQ ID NO: EE360-2
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA
 - (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
 - (iv) ORIGINAL SOURCE: HIV
 - (v) INDIVIDUAL ISOLATE: _____
 - (vi) IMMEDIATE SOURCE: _____
 - (vii) CLONE: _____
 - (viii) POSITION IN GENOME: Within Env Gene
 - (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE360-2

25 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

30 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA

35 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE360-3
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA

50

55

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(vii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE360-3

20 1 5 10 15
Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala
TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA ACT ATA CAT ATA GCA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile		
CCA CGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA		

35

³⁰ Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE367-1

(i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL ISOLATE: _____

(vi) IMMEDIATE SOURCE:

(vii) CLONE: _____

(viii) POSITION IN GENOME: Within Env Gene

(ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE367-1

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly
 TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

10 20 25 30
 Leu Gly Arg Thr Phe Tyr Thr Gly Glu Val Ile Gly Asp Ile
 CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE367-2

- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 25 (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- 30 (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- 35 (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE367-2

1 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly
 45 TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

50

55

20 25 30

Leu Gly Arg Thr Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile
 CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE367-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL ISOLATE: _____

(vi) IMMEDIATE SOURCE:

(vii) CLONE: _____

(viii) POSITION IN GENOME: Within Env Gene

(ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(x) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE367-3

35 1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly
 TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

40

20 25 30

Leu Gly Arg Thr Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile
 CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE370-1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA
 - (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
 - (iv) ORIGINAL SOURCE: HIV
 - (v) INDIVIDUAL ISOLATE: _____
 - (vi) IMMEDIATE SOURCE:
 - (C) CLONE: _____
 - (vii) POSITION IN GENOME: Within Env Gene
 - (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE370-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile
	CCA	GGA	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE370-2
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA

- 5 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 10 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 15 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 20 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE370-2

20 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

25 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGA AGA CCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

30 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 35 (2) INFORMATION FOR SEQ ID NO: EE370-3
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 40 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 45 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 50 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE370-3

1 5 10 15
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30
 10 Pro Gly Arg Ala Phe Tyr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35
 15 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE374-1

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 25 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 30 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 35 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic
 determinant
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE374-1

1 5 10 15
 45 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE374-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____

- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene

- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

- (viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE374-2

1 5 10 15

Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE374-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE374-3

25	1	5	10	15											
	Cys	Ile	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
	TGT	ATA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Thr	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	ACA	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE378-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

50

55

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE378-1

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly	TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA CGA		

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE378-2

(i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE378-2

1 5 10 15
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 15 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE378-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE378-3

1 5 10 15
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE380-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE380-1

35 1 5 10 15

Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

40 20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

(2) INFORMATION FOR SEQ ID NO: EE380-2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE380-2

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
	TGT	ACA	AGA	CCC	AGC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	CAA	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

40 (2) INFORMATION FOR SEQ ID NO: EE397-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

50

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- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

15 SEO ID NO: EE397-1

20 1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CAC ATA GGA

25	20	25	30
	Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asn Ile		
	CCA CGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA AAT ATA		

35

30 Arg Gln Ala Tyr Cys
AGA CAA GCA TAT TGC

- (2) INFORMATION FOR SEQ ID NO: EE399-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE399-1

5 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE399-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE399-2

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 45 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

50

55

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA CGA GAA ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE399-3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE399-3

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGT ATA CAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA CGA GAA ATA ATA GGA AAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE405-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE405-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Arg	Ile	Thr	Thr	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGA	ATA	ACT	ACG	GGA

30	20	25	30												
	Pro	Gly	Arg	Val	Tyr	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
	CCG	GGG	AGA	GTA	TAT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Lys	Ala	His	Cys
	AGA	AAA	GCA	CAT	TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE405-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

50

55

- 5 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 10 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 15 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 20 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

25 SEQ ID NO: EE405-2

1	5	10	15
Cys	Thr	Arg	Pro
TGT	ACA	AGA	CCC
			AAC
			AAC
			AAT
			ACA
			AGA
			AAA
			AGA
			ATA
			ACT
			ACG
			GGA

20	25	30												
Pro	Gly	Arg	Val	Tyr	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
CCG	GGG	AGA	GTA	TAT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

35				
Arg	Lys	Ala	His	Cys
AGA	AAA	GCA	CAT	TGT

- 35 (2) INFORMATION FOR SEQ ID NO: EE405-3
- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 45 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
- 50 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
- 55 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
- 60 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE405-3

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Lys Ile Thr Thr Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AAA ATA ACT ACG GGA

10 20 25 30
 Pro Gly Arg Val Tyr Tyr Thr Gly Glu Ile Ile Glu Asp Val
 CCG GGG AGA GTA TAT TAT ACA ACA GGA GAA ATA ATA GAA GAT GTA

15 35
 Arg Lys Ala His Cys
 AGA AAA GCA CAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE505-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE505-1

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AGT ATA AAT ATA GGA

20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAT ATA ACA GGA GAT ATA

5 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 10 (2) INFORMATION FOR SEQ ID NO: EE505-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

30 SEQ ID NO: EE505-2

35 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

40 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Thr Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAT ATA ACA GGA GAT ATA

45 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

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(2) INFORMATION FOR SEQ ID NO: EE505-3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE505-3

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Asn	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	AAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Thr	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAT	ATA	ACA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE507-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

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- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE507-1

1 5 10 15

²⁰ Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

20	25	30
25	Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile	CCA GGG AGA GCA TTT TAT GCA ACA CGA GAA ATA ATA GGA GAT ATA

Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE509-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE509-1

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA GGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCG GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE509-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE509-2

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA GGT ATA CAT ATA GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile	CCG GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA CGA GAT ATA	

5

35

10

(2) INFORMATION FOR SEQ ID NO: EE510-1

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL ISOLATE: _____

(vi) IMMEDIATE SOURCE:

 - (C) CLONE: _____

(vii) POSITION IN GENOME: Within Env Gene

(viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE510-1

35

1	5	10	15
Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly	TGT ACA AGA CCC AGT AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT		

40

20 25 30
 Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg
 CCA GGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA AGA

45

Gln Ala His Cys
GAA GCA GAT TCT

50

- (2) INFORMATION FOR SEQ ID NO: EE510-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE510-2

25 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CCC AGT AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT

30 20 25 30
 Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg
 CCA GGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA AGA

35 35
 Gln Ala His Cys
 CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE510-3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

50

55

- (ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE510-3

1 5 10 15

20 Cys Thr Arg Leu Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CTC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT

20	25	30
25	Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg	
	CCA GGA GCA TTT TAT ACA ACA CGA GAT ATA ATA GGA GAT ATA AGA	

30 Gln Ala His Cys
CAG GCA CAT TGT

35

40

45

50

- (2) INFORMATION FOR SEQ ID NO: EE520-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE: _____
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE520-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

- (2) INFORMATION FOR SEQ ID NO: EE520-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

- 5
 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved
 antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

10

SEQ ID NO: EE520-2

15
 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA CGA

20

20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

25

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

30

- (2) INFORMATION FOR SEQ ID NO: EE520-3
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 35 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 40 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved
 antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

50

55

SEQ ID NO: EE520-3

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGC

(2) INFORMATION FOR SEQ ID NO: EE528-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE: _____
- (c) CLONE: _____
- (vi) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION: _____

40 SEQ ID NO: EE528-1

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACG AGG AGA GGT ATA CAT ATA GGA

20 25 30

Pro Gly Arg Ala Val Tyr Ala Thr Asp Lys Ile Ile Gly Asn Ile
 CCA GGG AGA GCA GTT TAT GCA ACA GAT AAA ATA ATA GGA AAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE528-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE528-2

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACG AGG AGA GGT ATA CAT ATA GGA

40

20 25 30

Pro Gly Arg Ala Val Tyr Ala Thr Asp Lys Ile Ile Gly Asn Ile
 CCA GGG AGA GCA GTT TAT GCA ACA GAT AAA ATA ATA GGA AAT ATA

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35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

(2) INFORMATION FOR SEQ ID NO: EE528-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE: _____

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE528-3

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Gly	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACG	AGG	AGA	GGT	ATA	CAT	ATA	GGA

20	25	30												
Pro	Gly	Arg	Ala	Val	Tyr	Ala	Thr	Asp	Lys	Ile	Ile	Gly	Asn	Ile
CCA	GGG	AGA	GCA	GTT	TAT	GCA	ACA	GAT	AAA	ATA	ATA	GGA	AAT	ATA

35				
Arg	Gln	Ala	His	Cys
AGA	CAA	GCA	CAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE529-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

50

55

- 5
 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved
 antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

10 SEQ ID NO: EE529-1

15 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

20 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

25 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 30
 (2) INFORMATION FOR SEQ ID NO: EE529-2
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 35 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 40 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 45 (vi) PROPERTIES OF SEQUENCE: Expresses conserved
 antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

50 SEQ ID NO: EE529-2

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly	TGT ACA AGA CCT AAC AAT AAT ACA AGA AAA AGT ATA ACT ATA GGA		

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile		
CCG GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA		

35

(2) INFORMATION FOR SEQ ID NO: EE533-1

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE533-1

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly	TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA		

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA		

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

5

(2) INFORMATION FOR SEQ ID NO: EE533-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (vi) POSITION IN GENOME: Within Env Gene
- (vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

25

SEQ ID NO: EE533-2

30

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA

35

20	25	30												
Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile
CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAT	ATA	ATA	GGA	GAT	ATA

40

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

45

- (2) INFORMATION FOR SEQ ID NO: EE533-3
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

50

55

SEQ ID NO: EE533-3

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile	CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA	

35

(2) INFORMATION FOR SEQ ID NO: EE535-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein)

(A) SEQUENCE ASSEMBLY

(B) FRAGMENT TYPE: Individual

(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within

- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

5

SEQ ID NO: EE535-1

10 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

15 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

20 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE535-2

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

45

SEQ ID NO: EE535-2

50 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

55

20 25 30

Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

10

(2) INFORMATION FOR SEQ ID NO: EE543-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

- (E) INDIVIDUAL ISOLATE: _____

(v) IMMEDIATE SOURCE:

- (C) CLONE: _____

(vi) POSITION IN GENOME: Within Env Gene

(vii) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EE543-1

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

40

20 25 30

Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE543-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE: _____
- (vii) CLONE: _____
- (viii) POSITION IN GENOME: Within Env Gene
- (ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (x) SEQUENCE DESCRIPTION:

SEQ ID NO: EE543-2

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Thr	Ile	Gly
	TGT	ACA	AGA	CCC	AAT	AAC	AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

- (2) INFORMATION FOR SEQ ID NO: EE543-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment

(iii) (C) HYPOTHETICAL: _____
ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE543-3

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Thr	Ile	Gly
TGT	ACA	AGA	CCC	AAT	AAC	AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGG

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT CCA ACA CGA GAA ATA ATA GGA GAT ATA		

35

(2) INFORMATION FOR SEQ ID NO: E558-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA
(ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE558-1

1 5 10 15
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

15 35
 15 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGC

20 (2) INFORMATION FOR SEQ ID NO: EE558-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25 (ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

30 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

35 (v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE558-2

1 5 10 15
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Leu Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA GGG

20 25 30
 50 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGC

5

(2) INFORMATION FOR SEQ ID NO: EE558-3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE: _____
- (vi) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION: _____

25

SEQ ID NO: EE558-3

30

1	5	10	15
Cys	Thr	Arg	Pro
TGT	ACA	AGA	CCC
			AAC
			AAC
			AAT
			ACA
			AGA
			AAA
			AGT
			ATA
			CAT
			CTA
			GGG

35

20	25	30
Pro	Gly	Arg
CCA	GGG	AGA
		GCA
		TTT
		TAT
		ACA
		ACA
		GGA
		GAC
		ATA
		ATA
		GGA
		GAT
		ATA

40

35	
Arg	Gln
AGA	CAA

50

- (2) INFORMATION FOR SEQ ID NO: EE594-1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid

55

SEQ ID NO: EE594-1

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	MET	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	ATG	AAA	AGT	ATA	CAT	ATA	GGA

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile
 CGA CCC ACA GCA TTT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA

35

- (2) INFORMATION FOR SEQ ID NO: EE594-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
5 antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE594-2

10

1	5	10	15
Cys	Thr	Arg	Pro
TGT	ACA	AGA	CCC
Asn	Asn	Asn	AAC
Asn	Thr	MET	ACA
		Lys	ATG
		Ser	AAA
		Ile	AGT
		His	ATA
		Ile	CAT
		Gly	ATA

15

20	25	30
Pro	Gly	Arg
CCA	GGG	AGA
Gly	AGA	GCA
Arg	Ala	Phe
CCG	GGG	Tyr
		Thr
		Thr
		Gly
		Gln
		Ile
		Ile
		Gly
		Asp
		Ile

20

35	
Arg	Gln
Gly	Ala
Arg	His
AGA	CAA
	GCA
	CAT
	TGT

25

(2) INFORMATION FOR SEQ ID NO: EE594-3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
40 antigenic determinant

(viii) SEQUENCE DESCRIPTION:

45

SEQ ID NO: EE594-3

50

55

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr MET Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAT ACA ATG AAA AGT ATA CAT ATA GGA

5 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA

10 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 15
- (2) INFORMATION FOR SEQ ID NO: EE628-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- 35 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE628-1

40 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly
 TGT ACA AGA CCC AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA

45 20 25 30
 Pro Gly Lys Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile
 CCA GGG AAA GCA TTT TAT GCA ACA GGG GAC ATA ATA GGA AAT ATA

50

55

35

Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

5

(2) INFORMATION FOR SEQ ID NO: EE628-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

25

SEQ ID NO: EE628-2

30

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	MET	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	GGT	ATA	CAT	ATG	CGA

35

20	25	30												
Pro	Gly	Lys	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asn	Ile
CCA	GGG	AAA	GCA	TTT	TAT	GCA	ACA	GGG	GAC	ATA	ATA	GGA	AAT	ATA

40

35				
Arg	Gln	Ala	His	Cys
AGA	CAA	GCA	CAT	TGT

50

55

- (D) TOPOLOGY: Linear
 5 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 10 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 15 (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved
 antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE628-3

20 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA

25 20 25 30
 Pro Gly Lys Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile
 CCA GGG AAA GCA TTT TAT GCA ACA GGG GAC ATA ATA GGA AAT ATA

30 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

35 (2) INFORMATION FOR SEQ ID NO: EE639-1

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 45 (C) HYPOTHETICAL: _____
 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene
 - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - (viii) SEQUENCE DESCRIPTION:

5

SEQ ID NO: EE639-1

10

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	His	Thr	Glu	Lys	Arg	Ile	Thr	Leu	Gly
TGT	ACA	AGA	CCC	AAC	AAC	CAT	ACA	CAA	AAA	CGT	ATA	ACT	CTA	GGG

15

20	25	30
Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile	CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA	

20

35

25

(2) INFORMATION FOR SEQ ID NO: EE639-2

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

45

SEQ ID NO: EE639-2

50

55

(2) INFORMATION FOR SEQ ID NO: EE639-3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA
(iii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(v) IMMEDIATE SOURCE:
(C) CLONE: _____

(vi) POSITION IN GENOME: Within Env Gene
(vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE639-3

40 1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
TGT ACA AGA CCC AAC AAT ACA AGG AAA AGT ATA CCA ATA GGA

45 20 25 30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

50

55

154

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1 5 10 15
Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly
TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

5 20 25 30
Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile
CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA

10 35
Arg Arg Ala His Cys
AGA CGA GCA CAT TGT

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

5

(2) INFORMATION FOR SEQ ID NO: EE660-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iv) ORIGINAL SOURCE: HIV

(v) INDIVIDUAL ISOLATE: _____

(vi) IMMEDIATE SOURCE:

(vii) CLONE: _____

(viii) POSITION IN GENOME: Within Env Gene

(ix) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(x) SEQUENCE DESCRIPTION:

25

SEQ ID NO: EE660-1

30

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA

35

20	25	30												
Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Asp	Val	Ile	Gly	Asp	Ile
CCA	GGA	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAT	GTA	ATA	GGA	GAT	ATA

40

35				
Arg	Gln	Ala	Arg	Cys
AGA	CAA	GCA	CGT	TGT

45

(2) INFORMATION FOR SEQ ID NO: EE660-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

50

55

SEQ ID NO: EE660-2

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Asn	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	AAT	ATA	GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Ala Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTC TAT GCA ACA GGA GCC ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE661-1

(i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(iv) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

 - (C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
5 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE661-1

10 1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

15 20 25 30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

20 35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

- 25 (2) INFORMATION FOR SEQ ID NO: EE661-2
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105
(B) TYPE: Nucleic Acid
30 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) KIND: cDNA to genomic RNA
(iii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
35 (B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____
(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____
(iv) IMMEDIATE SOURCE:
(C) CLONE: _____
40 (v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
(viii) SEQUENCE DESCRIPTION:

45 SEQ ID NO: EE661-2

50

55

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA		

35

(2) INFORMATION FOR SEQ ID NO: EE661-3

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(iv) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

 - (C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE661-3

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Ser	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	TCT	ATA	GGA

20 25 30
Pro Gly Arg Ala Phe Phe Thr Thr Gly Gln Ile Ile Gly Asp Ile
CCA CGG AGA CCA TTTT TTTT ACA ACA GGA CAA ATA ATA CGA GAT ATA

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 5
- (2) INFORMATION FOR SEQ ID NO: EE663-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (v) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (vi) POSITION IN GENOME: Within Env Gene
- (vii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:
- 25

SEQ ID NO: EE663-1

30 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

35 20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

40 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 45
- (2) INFORMATION FOR SEQ ID NO: EE663-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- 50

SEQ ID NO: EE663-2

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly	TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA		

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA CGA AAT ATA		

35

(2) INFORMATION FOR SEQ ID NO: EE663-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(iv) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

- (C) CLONE: _____

- 5 (v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant
(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE663-3

10 1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile Thr Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA ACT ATA GGA

15 20 25 30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
CCA GGG AGA GCA TTT TAT CCA ACA GGA GAA ATA ATA GGA GAT ATA

20 35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

- 25 (2) INFORMATION FOR SEQ ID NO: EE665-1
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
30 (ii) KIND: cDNA to genomic RNA
(ii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____
35 (iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____
(iv) IMMEDIATE SOURCE:
(C) CLONE: _____
40 (v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant
(viii) SEQUENCE DESCRIPTION:

45 SEQ ID NO: EE665-1

50

55

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGT ATA CCT ATA GGA

5

20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA CAA ATA ATA GGA GAT ATA

10

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

15

(2) INFORMATION FOR SEQ ID NO: EE665-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iv) ORIGINAL SOURCE: HIV
- (v) INDIVIDUAL ISOLATE: _____
- (vi) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (vii) POSITION IN GENOME: Within Env Gene
- (viii) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (ix) SEQUENCE DESCRIPTION:

SEQ ID NO: EE665-2

40

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGT ATA CCT ATA GGA

45

20 25 30
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Ile Ile Gly Asp Ile
 CCA GGG AGA GCA TTT TAT GCA ACA GGA CAA ATA ATA GGA GAT ATA

50

55

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

5

(2) INFORMATION FOR SEQ ID NO: EE665-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

25 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE665-3

30

1	5	10	15
Cys	Thr Arg Pro Asn Asn Asn	Thr Arg Arg Ser Ile Pro Ile Gly	
TGT	ACA AGA CCC AAC AAC	ACA AGA AGT ATA CCT ATA GGA	

35

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT GCA ACA GGA CAA ATA ATA GGA GAT ATA		

40

	35	
Arg Gln Ala His Cys		
AGA CAA GCA CAT TGT		

45

(2) INFORMATION FOR SEQ ID NO: EE667-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

50

55

SEQ ID NO: EE667-1

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Arg	Ile	Thr	Thr	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGA	ATA	ACT	ACG	GGA

20	25	30
Pro Gly Arg Val Tyr Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCG GGG AGA GTA TAT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA		

35

- (2) INFORMATION FOR SEQ ID NO: EE667-2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

- (v) POSITION IN GENOME: Within Env Gene
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

5

SEQ ID NO: EE667-2

10 1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

15 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA

20 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAC TGT

- 25 (2) INFORMATION FOR SEQ ID NO: EE667-3
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 30 (ii) KIND: cDNA to genomic RNA
 (ii) KIND (if peptide or protein):
 (A) SEQUENCE ASSEMBLY METHOD: Overlap
 (B) FRAGMENT TYPE: Internal Fragment
 (C) HYPOTHETICAL: _____
 35 (iii) ORIGINAL SOURCE: HIV
 (E) INDIVIDUAL ISOLATE: _____
 (iv) IMMEDIATE SOURCE:
 (C) CLONE: _____
 (v) POSITION IN GENOME: Within Env Gene
 40 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 (viii) SEQUENCE DESCRIPTION:

45

SEQ ID NO: EE667-3

50

1 5 10 15
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

55

20 25 30

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA

5

35

Arg Gln Ala His Cys
 AGA CAA GCA CAC TGT

10

- (2) INFORMATION FOR SEQ ID NO: EE669-1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) KIND: cDNA to genomic RNA
 - (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
 - (iii) ORIGINAL SOURCE: HIV
 - (E) INDIVIDUAL ISOLATE: _____
 - (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
 - (v) POSITION IN GENOME: Within Env Gene
 - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
 - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE669-1

35

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
 TGT ACA AGA CCT AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

40

20 25 30

Pro Gly Arg Ala Ile Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA ATT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

45

35

Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

50

55

- (2) INFORMATION FOR SEQ ID NO: EE669-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE669-2

25
 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
 TGT ACA AGA CCT AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

30
 20 25 30
 Pro Gly Arg Ala Ile Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
 CCA GGG AGA GCA ATT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

- 40 (2) INFORMATION FOR SEQ ID NO: EE669-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment

(iii) (C) HYPOTHETICAL: _____
ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE669-3

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly	TGT ACA AGA CCT AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA		

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile	CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA	

35

(2) INFORMATION FOR SEQ ID NO: EE1476-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE1476-1

5 1 5 10 15
 Cys Thr Arg Pro Tyr Asn Asn Ile Lys Ile Arg Ser Ile His Ile
 TGT ACA AGG CCC TAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

10 20 25 30
 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg
 GCA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

15 35
 Gln Ala Tyr Cys
 CAA GCA TAT TGT

20 (2) INFORMATION FOR SEQ ID NO: EE3032-1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) IMMEDIATE SOURCE:
 - (C) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE3032-1

1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 45 TGT ACA AGG CCC AAT AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
 50 CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

5

(2) INFORMATION FOR SEQ ID NO: EE3032-2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____
- (iii) ORIGINAL SOURCE: HIV
- (iv) INDIVIDUAL ISOLATE: _____
- (iv) IMMEDIATE SOURCE:
- (c) CLONE: _____
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE3032-2

30

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn	Thr Arg Lys Gly Ile His MET Gly		
TGT ACA AGG CCC AAT AAC ACA AGA AAA GGT ATA CAT ATG GGA			

35

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA		

40

35		
Arg Gln Ala His Cys		
AGA CAA GCA CAT TGT		

45

- (2) INFORMATION FOR SEQ ID NO: EE3032-3
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

50

55

SEQ ID NO: EE3032-3

20	1	5	10	15
	Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly			
	TGT ACA AGG CCC AAT AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA			

25	20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile			
CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA			

30 Arg Gln Ala His Cys
AGA CAA GCA CAT TGT 35

35 (2) INFORMATION FOR SEQ ID NO: EEE6405-1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40 (ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

(A) SEQUENCE ASSEMBLY METHOD: Overlap

(B) FRAGMENT TYPE: Internal Fragment

(C) HYPOTHETICAL: _____

45 (iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

50 (v) POSITION IN GENOME: Within Env Gene

20	25	30
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile MET Gly Asp Ile		
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATG GGA GAT ATA		

5 35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEO ID NO: EE6405-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA
(iii) KIND (if peptide or protein):
(A) SEQUENCE ASSEMBLY METHOD: Overlap
(B) FRAGMENT TYPE: Internal Fragment
(C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6405-3

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGG	AAA	AGT	ATA	CCT	ATA	GGA

20	25	30
Pro Arg Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile	CCA AGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA CAT ATA	

35

(2) INFORMATION FOR SEQ ID NO: EE6636-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6636-1

25	1	5	10	15											
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	ACT	ATA	CAT	ATA	GGA

30	20	25	30												
	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Gl	Ile	Ile	Gly	Asn	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	AAT	ATA

35	35				
	Arg	Gln	Ala	His	Cys
	AGA	CAA	GCA	CAT	TGT

(2) INFORMATION FOR SEQ ID NO: EE6636-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment

- (iii) (C) HYPOTHETICAL: _____
ORIGINAL SOURCE: HIV
(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:
(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene
(vi) PROPERTIES OF SEQUENCE: Expresses conserved
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6636-2

1	5	10	15											
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile	CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA	

35

(2) INFORMATION FOR SEQ ID NO: EE6636-3

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 105
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

 - (A) SEQUENCE ASSEMBLY METHOD: Overlap
 - (B) FRAGMENT TYPE: Internal Fragment
 - (C) HYPOTHETICAL: _____

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: _____

(iv) IMMEDIATE SOURCE:

(C) CLONE: _____

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6636-3

5 1 5 10 15
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10 20 25 30
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

15 35
 Arg Gln Ala His Cys
 AGA CAA GCA CAT TGT

20 Claims

1. An antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, comprising an antigenic conjugate of the formula

25 (PND)_n~(Omp),
 or pharmaceutically acceptable salt thereof, wherein:
 PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;
 30 n indicates the number of polypeptides of PND covalently linked to Omp and is 1-50;
 ~ indicates covalent linkage;
 Omp is purified outer membrane proteosome of Neisseria,
 said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length;
 35 said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;
 said polypeptide having any of the sequences given in the sequence listing with the exception of sequence nos. EE90-1, EE90-2, EE90-3, EE312-1, EE360-1, EE360-2, EE360-3, EE667-3 and EE6405-3.
 40 2. The antigenic conjugate of claim 1 wherein X is proline.
 3. The antigenic conjugate of claim 1 wherein the covalent linkage between PND and Omp consists essentially of a bigeneric spacer.
 45 4. The antigenic conjugate of claims 1-3, in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.
 5. The antigenic conjugate of claims 1-3, wherein said Omp is derived from Neisseria meningitidis.
 50 6. A cocktail of antigenic conjugates consisting essentially of a mixture of more than one molecular species of the antigenic conjugates of claims 1-3.
 7. An AIDS vaccine comprising an antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, said conjugate of the formula
 (PND)_n~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

PNP is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n indicates the number of polypeptides of PNP covalently linked to Omp and is 1-50;

~ indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria;

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length;

said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing;

said conjugate mixed with a suitable immunological adjuvant, carrier or vector, said vaccine to be used pre- and post-exposure to prevent or treat HIV infection or disease, said vaccine capable of eliciting specific HIV neutralizing antibodies.

15 8. The AIDS vaccine of claim 7 wherein X is proline.

9. The AIDS vaccine of claim 7 wherein the covalent linkage between PNP and Omp consists essentially of a bigeneric spacer.

20 10. The AIDS vaccine of claims 7-9 in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.

11. The AIDS vaccine of claims 7-9, wherein said Omp is derived from Neisseria meningitidis.

25 12. The AIDS vaccine of claim 7-9 comprising a cocktail of said antigenic conjugates, said cocktail consisting essentially of a mixture of more than one molecular species of said antigenic conjugates.

30 13. A pharmaceutical composition comprising an antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, said antigenic conjugate of the formula

(PNP)n-(Omp),

or pharmaceutically acceptable salt thereof, wherein:

35 PNP is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n indicates the number of polypeptides of PNP covalently linked to Omp and is 1-50;

~ indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria,

40 said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length;

said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing;

said conjugate mixed with a suitable immunological adjuvant, said composition useful as a vaccine capable of producing specific HIV neutralizing antibody in mammals.

45 14. The composition of claim 13 wherein X is proline.

15. The composition of claim 13 wherein the covalent linkage between PNP and Omp consists essentially of a bigeneric spacer.

50 16. The composition of claims 13-15, in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.

55 17. The composition of claims 13-15, wherein said Omp is derived from Neisseria meningitidis.

18. A pharmaceutical composition containing a cocktail of antigenic conjugates consisting essentially of a mixture of more than one molecular species of the antigenic conjugates of claims 13-15.

19. The use of a conjugate as claimed in claim 1 for the preparation of a medicament for vaccinating against AIDS or ARC.
20. The use of a conjugate as claimed in claim 2 for the preparation of a medicament for vaccinating
5 against AIDS or ARC.
21. The use of a conjugate as claimed in claim 3 for the preparation of a medicament for vaccinating against AIDS or ARC.
- 10 22. The use of a conjugate as claimed in claim 1 together with any of the antivirals, immunolodulators or anti-infectives of Table I for the preparation of a medicament for vaccinating against AIDS or ARC.
23. The use as claimed in claim 19 or 20 wherein the Omp is derived from Neisseria meningitidis.
- 15 24. The use of a conjugate as claimed in claim 1 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
- 25 25. The use of a conjugate as claimed in claim 2 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
- 20 26. The use of a conjugate as claimed in claim 3 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
- 25 27. The use of a conjugate as claimed in claim 1 together with any of the antivirals, immunolodulators or anti-infectives of Table I for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
28. The use as claimed in claim 24 or 25 wherein the Omp is derived from Neisseria meningitidis.

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